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73 TCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 TCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.9
Matches 1107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 79, Appl
Sequence 79, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 48, Appl
Sequence 48, Appl
Sequence 19, Appl
Sequence 19, Appl
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Sequence 386, App
Sequence 86, Appl
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34, Appl
34, Appl
                                                                      3; Search time 80 Seconds (without alignments) 8303.453 Million cell updates/sec
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                                                                                                                                                    Sequence 86,
Sequence 79,
Sequence 79,
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Sequence 34,
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Sequence 4,
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Sequence 1
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-204-708-86
US-10-204-708-86
US-09-618-166-79
US-09-345-882-1
US-08-377-68-48
US-08-377-68-48
US-08-77-91-19
US-08-77-91-19
US-09-77-91-19
US-09-91-19
US-09-18-11-674
US-09-18-11-791
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                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-514-422-1
US-08-256-799-4
US-08-462-437-4
                                                                                                                                                                                                                  682709 segs, 277475446 residues
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                                                                        2004, 06:16:43
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                                                  sw model
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Gapop_60.0 , Gapext 60.0
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                                               nucleic search, using
                                                                                                                        US-10-063-730-115
1197
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Maximum DB seq length: 200000000
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Match Length
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11050
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No.
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US-09 US-09	t T. 96620312D ptides US/09/620,312l 07-19 9/552,317 25/52,317 25/52,317 26/88,725 21 00 1.0
1.9 1.9 1.9 1.9 1.9 553 4 1.9 653 4 1.9 976 1.9 976 1.9 976 1.9 100 1.9 100 1.9 11.9 11.9 11.9 11.9	lication US  2  ON:  Y. Tom  Chenghua  di, Vinod  G, Jie  Felyan  Rui-hong  Olng A.  Man, Tom  Man, Tom  Alan, Tom  Alan, Tom  Cling A.  Norghong  Vonghong  Els  ON NUMBER:  ON NUMBER:  ON NUMBER:  ON:  NUMBER:  ON:  NUMBER:  ON:  Els  Z000-04-  NUMBER:  ON:  NUMBER:  ON:  NUMBER:  ON:  Sapiens  Sapiens
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-09-620-312D-387 Sequence 387, Application Patent No. 6565962 GENERAL INFORMATION: APPLICANT: Tang, Y. Tom APPLICANT: Liu, Chenghua APPLICANT: Zhang, Jie APPLICANT: Zhang, Jie APPLICANT: Zhang, Jie APPLICANT: Zhao, Qing A. APPLICANT: Zhao, Qing A. APPLICANT: Zhao, Qing A. APPLICANT: Wehrman, Tom APPLICANT: Wehrman, Tom APPLICANT: Wehrman, Tom APPLICANT: Wang, Jian-Ru FEATURE: PLING DATE: 2000-0 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-0 PRIOR APPLICATION NUMBER: PRIOR APPLICATIO

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Gaps

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1;

0; Mismatches

88.3%; Score 1057; 99.9%; Pred. No. 0;

DB 4; Length 1380; Indels

us-10-063-730-115.olig10.rni

RESULT 2 US-0-620-312D-386 Sequence 386, Application US/09620312D FREER NO. 656962 RETERIN NO. 656962 RETERIN NO. 656962 PAPLICANT Tangy Y. Tom APPLICANT Asundi, Vinod APPLICANT Chenglua APPLICANT Chenglua APPLICANT Chen, Rui-hong APPLICANT Ren, Penivan APPLICANT Wong, Jian-Rui APPLICANT Wong, Jian-Rui APPLICANT Wong, Jian-Rui APPLICANT Wong, Jian-Rui APPLICANT Wong, Dunrui APPLICANT Wong, Dunrui APPLICANT Wong, Dunrui APPLICANT Wong, Dunrui APPLICANT WONG, POLYPEPTIGE APPLICANT WONG WONGER: 05/06/620.312D CURRENT PELLON NOWERR: 09/06/620.312D CURRENT PELLON DATE: 2000-07-19 FRICK REPERRNEE: 784C1P2B CURRENT PELLON DATE: 2000-07-19 FRICK REPERRNEE: 784C1P2B CURRENT PELLON DATE: 2000-07-19 FRICK REPERRNEE: 784C1P2B CURRENT PELLON DATE: 2000-07-19 FRICK REPERRNEE: 194C1P2B FRICK PELLON DATE: 2000-07-19 FRICK PERTURE: FRATURE: FRA	Query Match         45.7%; Score 547; DB 4; Length 1428;           Best Local Similarity 100.0%; Pred. No. 8.8e-240; Indels 0; Gaps 0;           Matches 547; Conservative 0; Mismatches 0; Indels 0; Gaps 0;           Qy 634 AGTITCTGGGTAGACTTGGGGGGGAGGAGTCTTCACTTTCCTGCCAACGA 813           Db 754 AGTITCTGGGTAGACAAGACTTGAGGAGGAGAGATCTTCACTTTCCTGCCAACGA 813           Qy 694 AAAAAAGGGATTGAACAAAGACTGGAGGAGAGATCTTCACTTTCCTGCCAACGA 813           Db 814 AAAAAAGGGATTGAACAAAGAGAGAGGGGGGGGGGGGGG
133 ATGTAAATCACTTAAGATTTGTGGACTGGTGTTTTGGTCTTGGCCCTAACTCAATTGT 192 205 ATGTAAATCACTTAAGATTTGTGGACTGGTTTTGGTACCTGGCCCTAACTCTAATTGT 264 205 ATGTAAATCACTTAAGATTTGTGGACTGGACGTACCCTAACTCTAACTTGT 264 206 ATGTTTTGGGGGAGCAACTCTGGCCGAGGTACCCAAAAAGCCTATGAACTGGA 322 265 CCTGTTTTGGGGGAGCAAGGCGAAGAGAAGAAGAAAAAGCCTATGAACTGGA 324 253 GCACACTTTCTACACCAATGGAAGAAGAAGAAGATTTACATGGAAATTGAACCACTGGA 332 313 CAGAACTGAAATTACAAAGCGGAAATGGCACTTTAACATGGAAATTGAACCACTTTTAACAAGAATTAACAAAATGAATTAACAAAATGAATTAACAAAATGAATTAACAAAAATGAAATTAACAAAAATGAAATTAACAAAATTAACAAAAATGAAATTAACAAAAATGAAATTAACAAAAATTAACAAAATTAACAAAATTAACAAAATTAACAAAAATTAACAAAAATGAAATTAACAAAAATGAAATTAACAAAAATGAAAAAATGAAAAAATGAAAAAATGAAAAAAAA	805   TCAGTGAAGTAGGAAGACCCGTCACGCAGCAAGGAGGAACTTCCAAT   864   865   TCAGTGAAGTAGGAAGACCCGTCACGCCAGCAAGGAGGAACTTCCAAT   864   865   AAATGACTATACTGAAAATGGAATTGATCCCATGCTGGATCAGAGGAACTTATG   824   865   AAATGACTATACTGAAAATGGAATTGATCCCATGCTGGATCAGAGGATATTG   924   865   AAATGACTATACTGAAAATGGAATAGAATTTGATCCCATGCTGGATCAGGAGGACGATATTG   924   865   TTGTATTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCCGCTCTTGTGAGG   912   925   TTGTATTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCTCTTGTGAGC   926   937   TTGTAACTGCCGTTACTGCTGCCCAGGAGGACGACACTCTGTCGTCTCATCATGC   936   937   TTGTAACTGCTGCTCATCATGCTGCCGCAGGAGGACGACTATTGAGCTCAAT   104   973   TTGTAACTGCTGGCTCAAAT   104   973   TTGTAACTGCTGGCTCACAGGAGGACGACGACTTACTGAGCTCAAT   104   973   TTGTAACTGCTGGCTCAAATAATAAATGCATGCTATTCAATGAATTTCTGCCTATGAG   1164   1161   1

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SEQUENCE CHARACTERISTICS
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US-09-618-166-79/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-781-891-79
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: PLEBENBROCK, Christian
APPLICANT: BITERNECK, Christian
APPLICANT: BERLIN, Kutt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dy Assessing DNA Methylation
TITLE OF INVENTION: Dy Assessing DNA Methylation
TITLE OF INVENTION: DOWNER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 86
IENGTH: 11050
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                                                1234 GCTCTCCAGAATTACTTGTAGGTAATTCCTCTTCATGTTCTAATAAACTTCTACATTA 1293
                       1054 TAATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 11050;
0.018;
hes 0; Indels
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APPLICANT: Yu, Chang-En
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Miligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
CORRESPONDENCE: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6100 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.2%; Score 26; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 26; Conservative 0; Mismatches
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Patent No. 6090620
GENERAL INFORMATION:
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; Sequence 86, Application US/10204708
; Patent No. 6677731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                               1114 GCTCTCCAGAATTACT
                                                                                                                                                                                                     TCACCAA 1180
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Washington
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Pred. No. 0.048;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: Seed Intellectual Property Law Group STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mulligan, John T.
Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED
WERNER'S SYNDROME
                                                                                        OFFERENTING SYSIEM:
CURRENT APPLICATION DATA:
APPLICATION NAME:
TILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTONREY/AGENT INPORMATION:
NAME: No. 609620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFRENCE/POCKET NUMBER: 240052.419
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
TELECOMMULCATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.0%; Pred. No. 0.0
Matches 25; Conservative 0; Mismatches
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FILING DATE: 17-Jul-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29899 TATCACCAAAAAAAAAAAAAAAA 29875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1172 TATCACCAAAAAAAAAAAAAAA 1196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 79, Application US/09618166 Patent No. 6583112 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fu, Ying-Hui
Yu, Chang-En
Oshima, Junko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           : 87350 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 87350 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
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NAME/KEY: UNGUETON: ULKLIOWININGE/KEY: UNGUETON: 33095

OCHER INFORMATION: UNKNOWN
NAME/KEY: UNGUETON: 33160

OCHER INFORMATION: UNKNOWN
NAME/KEY: UNGUETON: 34026

OCHER INFORMATION: UNKNOWN
NAME/KEY: UNGUETON: 34020

OCHER INFORMATION: UNKNOWN
NAME/KEY: UNGUETON: 39020

OCHER INFORMATION: UNKNOWN
NAME/KEY: UNGUETON: 39020

OCHER INFORMATION: UNKNOWN
NAME/KEY: UNGUETON: 42164

OCHION: 42164

OCHER INFORMATION: UNKNOWN
NAME/KEY: UNGUETON: 42164

OCHER INFORMATION: UNKNOWN
NAME/KEY: UNGUETON: 42469

OTHER INFORMATION: UNKNOWN
NAME/KEY: UNGUETON: 42769

OTHER INFORMATION: UNKNOWN
NAME/KEY: UNGUETON
NAME/KEY: U
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LOCATION: 5923
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 59242
OTHER INFORMATION: unknown
                                        LOCATION: 31206
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 31592
OTHER INFORMATION: unknown
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LOCATION: 63290
OTHER INFORMATION: unknown
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COTHER INFORMATION: unknown
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OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 68697
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LOCATION: 53384
OTHER INFORMATION: unknown
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LOCATION: 54684
OTHER INFORMATION: unknown
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LOCATION: 59215
OTHER INFORMATION: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        i LENGTH: 87350 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 79:
US-09-618-166-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 7421
OTHER INFORMATION: unknown NAME/KFY: unsure
LOCATION: 7427
OTHER INFORMATION: unknown NAME/KFY: unsure
LOCATION: 11609
OTHER INFORMATION: unknown NAME/KFY: unsure
LOCATION: 12609
OTHER INFORMATION: unknown
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LOCATION: 12742
OTHER INFORMATION: unknown
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LOCATION: 29370
OTHER INFORMATION: unknown
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LOCATION: 29422
OTHER INFORMATION: unknown
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LOCATION: 29979
OTHER INFORMATION: unknown
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LOCATION: 29980
OTHER INPORMATION: unknown
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LOCATION: 29981
OTHER INFORMATION: unknown
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LOCATION: 30136
OTHER INFORMATION: unknown
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OTHER INFORMATION: unknown
NAME/KEY: unsure
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OTHER INFORMATION: unknown
NAME/KEY: unsure
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: unsure
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OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
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LOCATION: 97122
OTHER INFORMATION: 99-1442-224
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OTHER INFORMATION: 5-148-352
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OTHER INFORMATION: 5-140-361
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OTHER INFORMATION: 5-135-198
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OTHER INFORMATION: 5-135-357
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OTHER INFORMATION: 5-145-24
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LOCATION: 72771..72817
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LOCATION: 146345
OTHER INFORMATION:
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THER INFORMATION:
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DIHER INFORMATION:
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INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: allele
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NAME/KEY: allele
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TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
CURRENT APPLICATION NUMBER: US 60/091,315
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-12-10
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Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 25; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: 99-1437-325
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OTHER INFORMATION: 5-124-273
FEATURE:
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OTHER INFORMATION: 5-127-261
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OTHER INFORMATION: 5-128-60
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COTHER INPORMATION: unknown
NAME/KEY: unsure
LOCATION: 79198
OTHER INPORMATION: unknown
NAME/KEY: unsure
LOCATION: 86336
OTHER INPORMATION: unknown
COTHER INFORMATION:
                                                                                                                 LOCATION: 68739
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 69785
OTHER INFORMATION: unknown
NAME/KEY: unsure
                                               unknown
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SOFTWARE: Patent.pm
SEQ ID NO 1
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ORGANISM: Homo sapiens
                   NAME/KEY: unsure
LOCATION: 68718
OTHER INFORMATION:
                                                          NAME/KEY: unsure
LOCATION: 68733
OTHER INFORMATION:
    OTHER INFORMATION:
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NAME/KEY: allele
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NAME/KEY: allele
                                                                                                        NAME/KEY: unsure
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                 NAME/KEY:
LOCATION:
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1173 ATCACCAAAAAAAAAAAAAAAAA 1197
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APPLICANT: CASDRAW, UPDERT W.
APPLICANT: TERRAS, FRANKY R.G.
APPLICANT: TERRAS, FRANKY R.G.
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 48, Application US/08377687
Patent No. 5538225
GENERAL INFORMATION:
APPLICANT: BROEKABET, WILLEM F.
APPLICANT: CAMMUE, BRUNO P.A.
APPLICANT: OSBORN, RUPERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D.C. COUNTRY: USA
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                                                                                                                                                                                                                             NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
                                                                                                                                                                                                                                                                                                                          NAME/KEY: allele
LOCATION: 90819..90865
OTHER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: allele
LOCATION: 97099..97145
OTHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: allele
LOCATION: 97099..97145
FEATURE INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
FEATURE:
                                                                                                                                                             LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: allele
LOCATION: 97139..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
                                       NAME/KEY: allele
LOCATION: 88050..88096
OTHER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: allele
LOCATION: 97130..97177
OTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: allele
LOCATION: 99075..99121
JTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
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LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
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MAMB/KEY: allele
LOCARION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: allele
LCCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: allele
LOCATION: 93690..93736
OTHER INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
FEATURE:
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LOCATION: 103783...103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ
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DIHER INFORMATION: polymorphic fragment 5-130-257 SEQ
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LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395
                                                                                                              FEATURE:
NAME/KEY: allele
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NAME/KEY: allele
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NAME/KEY: allele LOCATION: 106918..106966 OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58

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NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
                                                                    FEATURE:
NAME/KEY: allele
LOCATION: 108084...108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
FEATURE:
                                                                                                                                                                                                                                                                                        NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
                                                                                                                                                                                                                                                    SEQ ID39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAN-1993
ATTORNEY,AGENT INFORMATION:
NAME: KONCLIES, PADI N.
REGITAATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPREATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CARRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                            NAME/KEY: allele
LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151927 ATCACCAAAAAAAAAAAAAAA 151903
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INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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MOLECULE TYPE:
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TOPOLOGY: linear MOLECULE TYPE: cDNA
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                            US-08-971-982-48
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100.0%; Pred. No. 0.16;
iive 0; Mismatches 0; Indels
                                                                                      2.0%; Score 24; DB 1; Length 414;
100.0%; Pred. No. 0.16;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/777,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: KOKULIS, PAUL N. REGISTRATION NUMBER: 16,773 REFERENCE/DOCKET NUMBER: 99042/SEE.36525/US/A
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BROEKABRI, WILLEM F.
APPLICANT: CAMUNE, BRUNO P.A.
APPLICANT: CSBORN, RUPERT W.
APPLICANT: REES, SARAH B.
APPLICANT: TERBAS, FRANKY R.G.
APPLICANT: VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1174 TCACCAAAAAAAAAAAAAAAAAAA 1197
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                                                                                                                                                                         1174 TCACCAAAAAAAAAAAAAAAAAAAAAAA 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CUSHMAN DARBY & CUSHMAN
                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSBE: CUSHMAN DARBY & CUSHMAN STREET: 1100 NEW YORK AVENUE, N.W. CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,480
FILING DATE: 04-JAM-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                           ; Sequence 48, Application US/08777192; Patent No. 5824869
; GENERAL INFORMATION:
; APPLICANT: BROEKABRT, WILLEM F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 202-861-3000
TELEPAX: 202-822-0944
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 414 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.0°
Best Local Similarity 100.
Matches 24; Conservative
                                                                                                             Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
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                                       16..255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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US-08-777-192-48
FEATURE:
NAME/KEY:
LOCATION:
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US-08-777-192-48
                                                         US-08-377-687-48
                                                                                                 Query Match
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971.982
FILING DATE: 17-00. 6187904-1997
CLASSIFICATION NUMBER: US 08/02,480
APPLICATION DATA:
APPLICATION DATA:
ANAME: CONCILS, PAUL N.
REGISTRATION: PRORMATION:
NAME: KOCKLIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 16,773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
2.0%; Score 24; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                              STREET: 1100 NEW YORK AVENUE, N.W.
                                                                                                                                               REES, SARAH B.
TERRAS, FRANKY R.G.
VANDERLEYDEN, JOZEF
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 16..255
SEQUENCE DESCRIPTION: SEQ ID NO: 48:
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APPLICANT: De Samblanx, Genoveva
APPLICANT: Brockaert, Willem
APPLICANT: Rees, Sarah
TILLE OF INVENTION: Antifungal Proteins
FILE REFERENCE: PPD50093
CURRENT APPLICATION NUMBER: US/09/077,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1174 TCACCAAAAAAAAAAAAAAAA 1197
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                                                                                                                                                                                                                                                                                            ADDRESSEE: CUSHMAN DARBY &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
TELEFAX: 202-822-0944
INFORMATION FOR SEQ ID NO: 48:
                                                                        APPLICANT: BROEKAERT, WILLEM F. CAMMUE, BRUNO P.A. OSBORN, RUPERT W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-077-951-19
; Sequence 19, Application US/09077951
; Patent No. 6372888
; Sequence 48, Application US/08971982; Patent No. 6187904; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 414 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
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US-08-123-161A-11

Sequence 11, Application US/08123161A

Patent No. 5446516

GENERAL INFORMATION:
APPLICANT: Campbell, Kevin P.
APPLICANT: Roberds, Steven L.
APPLICANT: Integration, Richard D.
APPLICANT: Integration, Oxana B.
APPLICANT: Anderson, Richard D.
APPLICANT: Wang, Bin
TITLE OF INVENTION: NUCLEIC ACID ENCODING DYSTROPHIN-ASSOCIATED
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0:
                                      APPLICANT: Bushnell, Steven E.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Catino, Theodore J.
APPLICANT: Derti, Adnan
APPLICANT: Derti, Adnan
APPLICANT: Ford, Donna M.
APPLICANT: Ford, Donna M.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
CURRENT APPLICATION NUMBER: US 60/088,801
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-08
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.0%; Score 24; DB 3; Length 705; 100.0%; Pred. No. 0.16; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRAIN COUNTRAIN COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
CORPETATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/123,161A
PTILING DATE: 16-SEP-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1174 TCACCAAAAAAAAAAAAAAAAA 1197
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NAME/KEY: misc_feature

LOCATION: (1)...(705)

OTHER INFORMATION: n = A,T,C or G
                     Burgess, Christopher C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/946,234
FILING DATE: 14-SEP-92
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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CURRENT FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: GB 9525474.4
EARLIER FILING DATE: 1995-12-13
EARLIER PEPLICATION NUMBER: PCT/GB96/03065
NUMBER OF SEQ ID NOS: 77
SEQ ID NO 19
LENTH: 414
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CURRENT APPLICATION WUMBER: U3/09/077,948A
CURRENT APPLICATION WUMBER: U3/09/077,948A
CURRENT APPLICATION WUMBER: PCT/GB96/03/068
PRIOR APPLICATION WUMBER: PCT/GB96/03/068
PRIOR APPLICATION WUMBER: GB 96.6552.9
PRIOR APPLICATION WUMBER: GB 9525455.3
NUMBER OF SEQ ID NOS: 141
SOFTWARE: FASTSEQ for Windows Version 4.0
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Pred. No.
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US-09-328-111-674/C
US-09-328-111-674/C
Sequence 674, Application US/09328111
Fatent No. 626233
GENERAL INFORMATION:
APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 45, Application US/09077948A
Patent No. 6605698
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Borremans, Frans
Borremans, Frans
Sitjtsma, Lolke
Meloen, Robbert
Pujjk, Wouter
Schaaper, Wilhelmus
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Best Local Similarity 100.0%; P.
Matches 24; Conservative 0;
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Van Gelder, Wilhelmus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Van Amerongen, Aart
                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Raphanus sativus
US-09-077-951-19
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Best Local Similarity 100.0
Matches 24; Conservative
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ORGANISM: Raphanus sativus
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APPLICANT:
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APPLICANT:
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APPLICANT:

à Пр NAME: Farrell, Kevin M.
REGISTRATION NUMBER: 35,505
REFERENCE/DOCKET NUMBER: UIRF89-11A4

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Gaps

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Sequence 11, Application US/08483278

Patent No. 5686073

GENERAL INFORMATION:
APPLICANT: Campbell, Kevin P.
APPLICANT: Leveille, Cynthia J.
APPLICANT: Leveille, Cynthia J.
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRES: 15
CORRESPONDENCE ADDRESS: ADDRESSEE: Kevin M. Farrell, P.C.
STREET: P.O. Box 999
CITY: York Harbor
STATE: ME
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COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRINY APPLICATION DATA:
APPLICATION NUMBER: US/08/483,278
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,161
FILING DATE: 16-SEP-93
ATTORNEY/AGENT INFORMATION:
RESTRATION NUMBER: 35,505
REPERADORS: (207) 363-0558
TELEPHONE: (207) 363-0558
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
TEMPORALION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPAX: (207) 363-0558
TELEPAX: (207) 363-0528
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1396 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Matches 24; Conservative
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; LOCATION: 4..1164
US-08-123-161A-11
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US-08-483-278-11
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US-08-483-278-11
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 Query Match
Best Local Similarity 100.(
Matches 24; Conservative
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Search completed: September 3, 2004, 07:45:39 Job time : 82 secs

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LOCATION: (13]
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Sequence 7, Appli
Sequence 14, Appl
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                                                         September 3, 2004, 04:36:32 ; Search time 80 Seconds
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(cgn2_6/ptodata/2/ina/5A_COMB.seq:*
(cgn2_6/ptodata/2/ina/5B_COMB.seq:*
(cgn2_6/ptodata/2/ina/6A_COMB.seq:*
(cgn2_6/ptodata/2/ina/6B_COMB.seq:*
(cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
(cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-241-465B-6
US-08-241-465B-6
US-08-241-465B-4
US-08-047-033-6
US-08-047-033-5
US-08-047-033-3
US-08-047-033-3
US-08-047-033-3
US-08-047-033-3
US-08-241-465B-7
US-08-241-465B-7
US-08-241-465B-7
US-08-241-465B-7
US-08-047-033-7
US-08-047-033-7
US-09-621-976-10374
US-09-573-906-1
US-09-134-001C-2521
US-09-134-001C-2521
US-09-134-001C-2521
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US-09-528-706-3
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Maximum Match 100%
Listing first 45 summaries
                                        - nucleic search, using sw model
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Maximum DB seq length: 200000000
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No.
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Sequence 17, Appl
Sequence 17, Appl
Sequence 1183, Ap
Sequence 1354, Ap
Sequence 5, Appli
Sequence 45, Appli
                                                                                                                                                                                     Sequence 2813. Apple Sequence 1, Appli Sequence 1, Appli Patent No. 5213972 Sequence 31, Appl Sequence 72, Appl Sequence 8100, Appl Sequence 6, Appli
 Sequence 64, Appl
Sequence 1, Appli
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Sequence 17, Appl
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               US-08-916-421B-1

US-09-023-942A-9

US-09-077-384-16

US-09-244-796-17

US-09-543-681A-1183

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US-09-134-001C-1354

US-09-134-001C-1354

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 387, Application US/09620312D Patent No. 6569662 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Zhang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Ren, Feiyan
APPLICANT: Wehrman, Tom
APPLICANT: Yang, Yonghong
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: May, Yunqing
APPLICANT: May, Yunqing
APPLICANT: Wang, Ding
APPLICANT: Wang, Ding
APPLICANT: Wang, Zhiwei
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Matches 1177; Conservative
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1686
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ORGANISM: Homo sapiens
RESULT 1
US-09-620-312D-387
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                                                                                                                                                                                                                                                                                                                                                                  AGAACTTCCAATAAATGACTATACTGAAAATGGAATAGAATTTGATCCCATGCTGGATGA
GGCAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAA
                                                                                                                AACTCTAATTGTCCTGTTTTGGGGGGGGGCACTTCTGGCCGGAGGTACCCAAAAAAGC
                                                                                                                                CTATGACATGGAGCACACTTTCTACAGCAATGGAGAAGAAGAAGAAGTTTACATGGAAAT
                                                                                                                                                                                                                              TGATCCTGTGACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGA
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TGATCCTGTGACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGA 360
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1213 CCTCTCTTCAFGTTCTAATAAACTTCTACATTATCACCAACA 1254
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APPLICANT: ABRING, VIENDA
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Xue, Aidong J.
APPLICANT: Xue, Aidong J.
APPLICANT: Xue, Vonghong J.
APPLICANT: Ang, Yunding
APPLICANT: Ang, Yunding
APPLICANT: Ang, Dunrui
APPLICANT: And Yunding
APPLICANT: Dramanac, Radoje T.
APPLICANT: Dramanac, Radoje T.
APPLICANT: Dramanac, Radoje T.
APPLICANT: Printinghast
APPLICANT: PAPLICATION NUMBER: 0569662el Nucleic Acids and
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: NO. 656962el Nucleic Acids and
TITLE OF INVENTION: NO. 656962el Nucleic Acids and
TITLE OF INVENTION: NO. 656962el Nucleic Acids and
TITLE OF INVENTION: NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
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PRIOR PRI
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Pred. No. 1.2e-311;
0; Mismatches 5;
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Best Local Similarity 95.73
Matches 1177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
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; LOCATION: (131)..(1132)
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ORGANISM:
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                                                                  GAATGAAGAAATTACCACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAA
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                                                TATCAAAACTCAGATTAAAGTGATTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGA
                                                                                                                        553 GAATGAAGAAATTACCACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAA
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Sequence 3, Application US/08241465B Patent No. 5719125

GENERAL INFORMATION:

Yuji HIRAKI Kazuhiro TAKAHASHI Junko SUZUKI Jun KONDO

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Fujio SUZUKI

Atsuko KOHARA

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179 GGGCCTTCTACTTCTGGAAGGGGAGCGACACTCACATTTACAATGTCCATTACACCATG 238
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                                                                                                        ADDALLS
STREET: 805 r.L.
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
) OPERATIG SYSTEM: PC-DOS/MS-DOS
SOFTWARE PARENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/241,465B
FTLING MAP 11, 1994
FTLING MAP 11, 1994
APPLICANT: Akiko MORI
APPLICANT: E: YAMADA
TILLE OF THOUSTION: HUMAN CHONDROMODULIN-I PROTEIN
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human being (Homo Sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.3%;
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LENGTH: 1006 base pairs
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IDENTIFICATION METHOD:
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APPLICANT: Yuji HIRAKI
APPLICANT: Yuji HIRAKI
APPLICANT: Yuji HIRAKI
APPLICANT: Junko SUZUKI
APPLICANT: Junko SUZUKI
APPLICANT: Atsuko KOHARA
APPLICANT: Atsuko KOHARA
APPLICANT: Atsuko MORI
APPLICANT: Bi YAMADA
TITLE OF INVENTION: HUMAN CHONDROMODULIN-I PROTEIN
NUMBER OF SEQUENCES: 21
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CURRENT APPLICATION DATE: US/08/241,465B
FILING DATE: May 11, 1994
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805 Fifteenth Street, N.W., #700
                                                                                                                                                             GTCCCTCAAGTGAAAGTAGAGAAGACCCGT-
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5719125
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SLECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-8850
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ATTORNEY/AGENT INFORMATION:
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0; Mismatches 396;
                                               TOPOLOGY: linear
ORIGINAL SOURCE:
ORGANISM: Human being (Homo Sapiens)
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Matches 411; Conservative
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double
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CLONE: phcHM-I3-6
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CGTATTCCTGAGGTGGCGCCGTGACCAAACAGAGCATCTCCTCCAAACTGGAAGGCAAG 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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805 Fifteenth Street, N.W.,
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FILING DATE: May 11, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: VIJI HIRAKI
APPLICANT: Kazuhiro TAKAHASHI
APPLICANT: Junko SUZUKI
APPLICANT: Junko SUZUKI
APPLICANT: Atsuko KOHARA
APPLICANT: Atsuko MORI
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NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
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MEDIUM TYPE: Floppy disk
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RY: D.C.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,465B
FILING DATE: WAY 11, 1994
CLASSIFICATION: 435
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Pred. No. 9e-21;
0; Mismatches 398;
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805 Fifteenth Street, N.W., #700
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ORGANISM: Human being (Homo Sapiens)
                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                             Sequence 6, Application US/08241465B Patent No. 5719125
GENERAL INFORMATION:
                                                                                                   Yuji HIRAKI
Kazuhiro TAKAHASHI
Junko SUZUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Warren M. Cheek, Jr.
RATION NUMBER: 33,367
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 1006 base pairs
                                                                                                                                                                        Atsuko KOHARA
Akiko MORI
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US-08-241-465B-6
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                                                                                   Fujio SUZUKI
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EDNESS: double
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                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                        TITLE OF INVENTION: HUNDMER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                        Jun KONDO
                                                                                                                                                                                                           Ei YAMADA
                                                                                                                                                                                                                                                                                                           CITY: Washington COUNTRY: D.C. ZIP: 20005
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LOCATION: 2 ...
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                US-08-241-465B-6
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896 CCCCTGGGGGGTATTACCCATGGCCTTATAATTATCAAGGCTGCCGTTCGGCCTGCAGA 955
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APPLICATION NUMBER: US/08/241,465B
FILING DATE: May 11, 1994
                                                                                                                                                                            Sequence 4, Application US/08241465B
Patent No. 5719125
GENERAL INFORMATION
APPLICANT: Fujio SUZUKI
APPLICANT: Yuji HIRAKI
                                                                                                                                                                                                                                        Fujio SUZUKI
Yuji HIRAKI
Kazuhiro TAKAHASHI
Junko SUZUKI
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NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-8850
                                                                                                                                                                                                                                                                                                                Jun KONDO
Atsuko KOHARA
Akiko MORI
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nucleic acid
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IDENTIFICATION METHOD:
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ORGANISM: Hum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAAACCGAGATTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATG 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            539 AAGGACAACAGCTTCTTGAG---TTCTAAGGTGTTAGAACTCTGCGGTGACCTTCCTATT 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGATCTTCACTTTCCTGCCAACGAAAAAAAAGGGATTGAACAAAATGAACAGTGGGTG 727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  479 ATCATGCCAGTCAAATATGAAGAAAATTCTCTTATCTGGGTGGCTGTAGATCAGCCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCCCTCAAGTGAAAGTAGAAGACCCGT-----CACGCCAGACAAGCAAGTGAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           716 GGAAGACTGAATGAAGCCAGACCCAGTGTTCAAGAGGACTCACAAGCCTTCAATCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         842 AGAGGITATIGITGIATTIACIGCCGICGAGGCAACCGCIAITGCCGCCGCGCTCTGIGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 GGGGCCTTCTACTTCTGGAAGGGGAGCGACAGTCACATTTACAATGTCCATTACACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263 TACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAGAACTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                              Length 1006;
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                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                            Score 104.6; DB 1;
Pred. No. 2.6e-20;
0; Mismatches 399;
                                                                                                                                                                                                                                            Human being (Homo Sapiens)
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-8850
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                            atch 8.7%;
cal Similarity 49.1%;
408; Conservative (
                                                                                                      INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1006 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                  , LOCATION: P CDS
, LOCATION: 2 .. 1003
, IDENTIFICATION METHOD: US-08-241-465B-5
                                                                                                                                                                                                          linear
                                                                                                                                                                                                          TOPOLOGY: lin
ORIGINAL SOURCE
                                                                                                                                                                                                                                            ORGANISM:
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Matches
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699 CATTCGACCCTAGACTGGATCACGAAGGAATCTGTTGTATAGAATGTAGGGGGGAGCTACA 758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    639 AGGACTCACAAGCCTTCAATCCTGATAATCCTTATCATCAGCAGGAAGGGAAAGCATGA
956 grearcareceareracerecerecececerarerrececareceres 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BI YAMADA
TITLE OF INVENTION: HUMAN CHONDROMODULIN-I PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.6%; Score 90.8; DB 1; Best Local Similarity 59.8%; Pred. No. 2.3e-16; Matches 152; Conservative 0; Mismatches 102;
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806 GAAAATGGAATTTGATCCCATGCTGGATGAGGAGGTTATTGTTGTTTTACTGC 865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  866 CGTCGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCATAT 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 AGGAGGAGCTACACCCACTGCCAGAAGATCKKNGAGCCTCTGGGGGGCTACCACCCATGG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCATACTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTGTAACTGGTGG 985
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US-08-047-033-5

Sequence 5, Application US/08047033

Patent No. 5444157

GENERAL INFORMATION:

APPLICANT: Fujio SUZUKI et al.

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSE: Wenderoth, Lind & Ponack

STRET: 805 Fifteenth Street, N.W., #700

CITY: Washington

STATE: D.C.

COMPUREY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb

COMPUTER: IBM Compatible

COMPUTER: IBM Compatible
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,033
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/821,859
                                                                                                                                                                                                                                                                   "N 1S T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DATE:
DOCUMENT NUMBER:
FILING DATE:
PRELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                             NAME/KEY: modified site
LOCATION: 249
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "N
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 63.8
Matches 132; Conservative
   POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
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                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL:
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                                                                                                                                                                                                                                                                                                                                                                      TITLE
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                                                          759 cccacrdccagaagarcrdrgaaccccrgggggcrarracccarggccrraraarrarc 818
                                                                                                                              Sequence 6, Application US/08047033
Fatent No. 5444157
GENERAL INFORMATION:
TITLE OF INVENTION: CHONDROMODULIN-I PROTEIN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS: 3
ADDRESSE: ADDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IRM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PPLICATION NUMBER: US/07/821,859
FILING DATE:
APPLICATION NUMBER: US/07/745,497
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fetal cartilage
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                                                                                                                                                                                                                                                                                                                          879 redecarecreraa 892
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SEQUENCE CHARACTERISTICS:
LENGTH: 363 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE: fetal of CELL TYPE:
CELL LINE:
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INDIVIDUAL ISOLATE:
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IMMEDIATE SOURCE:
LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-047-033-6
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ATTORNEY/AGENT INFORMATION:

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Sequence 4, Application US/08047033

Patent No. 5444157

GENERAL INFORMATION:
APPLICANT: Pujio SUZUKI et al.
IITLE OF INVENTION: CHONDROMODULIN-I PROTEIN
NUMBER OF SEQUENCES: 12

COMBERSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /note= "N is T, G, A or C"
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                    ZIP: 20005
COMPUTER READABLE FORM:
MBDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/07/745,497
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DCOKET NUMBER:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECHERAX: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/821,859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 365 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: modified site LOCATION: 251 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: DisplayWrite CURRENT APPLICATION DATA: APPLICATION NUMBER: US/
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HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: bovine
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MAP POSITION:
UNITS:
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POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                  JS-08-047-033-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218 AGAGGAGCTACACCCACTGCCAGAAGATCKKWGAGCCTCTGGGGGGCTACCACCCATGG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 GGAGAAAGCATGACATTCGACCCCAGACTGGATCATGAAGGAATCTGCTGTATAGAATGC 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: modified site
LOCATION: 250
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "N is T, G, A or C"
AUTHORS:
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; RELEVANT RESIDUES IN SEQ ID NO:
US-08-047-033-5
NAME: Warren M. Cheek Jr.
REGIEVRAIDON NUMBER: 33,367
REFRENCE, DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8856
TELEPAK: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HARLOTYPE:
TISSUE TYPE: fetal cartilage
                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 364 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                        ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: bovine
                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOCUMENT NUMBER
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                            Query Match 7.5%; Score 90; DB 1; Length 365; Best Local Similarity 63.8%; Pred. No. 2.5e-16; Matches 132; Conservative 2; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-047-033-3
; Sequence 3, Application US/08047033
; Patent No. 5444157;
Patent No. 5444157.

GENERAL INFORMATION:
TITLE OF INVENTION: CHONDROMODULIN-I PROTEIN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STRET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
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MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
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CLASSIFICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/821,859
FILING DATE:
APPLICATION NUMBER: US/07/745,497
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WALFEN M. CHEEK Jr.
REFERENCE/DOCKET NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,033
                                                                                           DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEYANT RESIDUES IN SEQ ID NO:
US-08-047-033-4
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 base pairs
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TITLE:
JOURNAL:
                                        VOLUME:
ISSUE:
PAGES:
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806 GAAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGGGTTATTGTTGTTTACTGC 865
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; Patent No. 5719125
; GENERAL INFORMATION:
; APPLICANT: Pujio SUZUKI
; APPLICANT: Kazuhiro TAKAHASHI
; APPLICANT: Junko SUZUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOCUMENT NUMBER:
FILING DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                 TISSUE TYPE: fetal cartilage
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: modified site
TACATION: 252
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Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 252
IDENTIFICATION METHOD:
OTHER INFORMATION: /nc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUBLICATION INFORMATION: AUTHORS:
nucleic acid
DNESS: single
                                                                                                                                                                                                     INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                 ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: bovine
                                         TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                            POSITION IN GENOME:
CHROMOSOME/SEGMENT
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
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US-08-047-033-3
                                                                                                                                                                                        STRAIN:
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                APPLICANT: Atsuko KOHARA
APPLICANT: Atkiko MORI
APPLICANT: Ei YAMADA
TITLE OF INVENTION: HUMAN CHONDROMODULIN-I PROTEIN
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM FC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,465B
FILING DATE: May 11, 1994
CLASSIFICATION: 435,
                                                                                                                                   3: Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Human being (Homo Sapiens)
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                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REPERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGGGAGGGTCTAA 1012
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SEQUENCE CHARACTERISTICS:
LENGTH: 892 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 2 . 889
IDENTIFICATION METHOD:
                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
Jun KONDO
                                                                                                                                                                     CITY: Washington
COUNTRY: D.C.
ZIP: 20005
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ORIGINAL SOURCE:
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                                                                                                                                   ADDRESSEE:
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Best Local S
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435 ITAAAGTGATTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAAGAAATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          615 TCAATCCCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGAGGAGAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           495 CCACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.4%; Score 53.2; DB 1; Length 7218; Best Local Similarity 4.1%; Pred. No. 4.5e-05; Matches 16; Conservative 216; Mismatches 154; Indels 0
                                                                                                                                                                                                                         ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/232,463
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTONNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTATION NUMBER: 29,768
                                                                                                                           ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         795 ATGACTATACTGAAAATGGAATAGAA 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 899149
INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: FINGTH: 7218 base pairs
                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                       STATE: V. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-232-463-14
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us-10-063-730-115.rni

Sequence 7, Application US/08047033

Sequence 7, Application US/08047033

GENERAL INFORMATION:
APPLICANT: FUJIO SUZUKI et al.
TITLE OF INVENTION: CHONDROWODULIN-I PROTEIN
NUMBER OF SEQUENCES: 12
CORRESPONDES 12
CORRESPONDE Menderoch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: INW Compatible
OPERATING SYSTEM: MS-DOS 1099 RRRRRRRRRRRRRRRRRRR 1074 FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
FILING DATE:
FILING DATE:
APPLICATION NUMBER: US/07/821,859
FILING DATE: SOFTWARE: DisplayWrite CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/047,033 TISSUE TYPE: fetal cartilage CELL TYPE: CELL LINE: ORGANELLE: IMMEDIATE SOURCE: LIBRARY: FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WALTEN M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/OFCET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850 LENGTH: 290 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: TELEFAX: 202-371-8856 STRAIN: INDIVIDUAL ISOLATE: DEVELOPMENTAL STAGE: MOLECULE TYPE: CDNA HYPOTHETICAL: POSITION IN GENOME: CHROMOSOME/SEGMENT MAP POSITION: FRAGMENT TYPE: ORIGINAL SOURCE: ORGANISM: bovine US-08-047-033-7 ANTI-SENSE: CLONE: g

0 806 GAAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGGGTTATTGTTGTATTTACTGC 865 866 CGTCGAGGCAACCGCCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATAT 925 217 AGAAGAAGTACACCCACTGCCAGAAGATCTGTGAGCCTCTGGGGGGCTACCACCATGG 276 Gaps Plunkett, Guy
Walch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison . 0 Query Match
4.1%; Score 49.2; DB 1; Length 290;
Best Local Similarity 60.4%; Pred. No. 0.00013;
Matches 81; Conservative 0; Mismatches 53; Indels ZIF: 53701-2113 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage NAME: Seay, Nicholas J.
REGISTRATION UNBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION: COMPUTER: IBM PC compatible
COMPAGE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION: RESULT 15
US-09-453-702B-14
US-09-453-702B-14
Sequence 14, Application US/09453702B
Patent No. 6365723
GENERAL INFORMATION:
HAPPLICANT: Blattner, Frederick R.
Frederick R.
Perna, Nicole T. (608) 251-5000 08) 251-9166 DATE:
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-047-033-7 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: 926 CCATACTGCTACCA 939 277 CCCTATAACTACCA 290 LENGTH: 12886 TYPE: nucleic acid UBLICATION INFORMATION: TELEPHONE: (60 TELEFAX: (608) STATE: WI COUNTRY: US JOURNAL: VOLUME: AUTHORS: ISSUE: PAGES: ð g ö g G δ

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1;
                                                                                                                                                                                                                                   3343 CAAAAAGAAAGTCTGAATTTAAATTCCTTTTAACTCAGAGAGATGATCCTACTTAGC 3402
                                                                                                                                                                                                                                                                                                                                                                            3403 AGAAAAACCCAATAAAAAAAGCCAGATATTTTTAAAAAATC-CAATTGCCAATATTTATGA 3461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3462 GGAATTGAAGNGCAATTTATTTATCCTGAATANGANCCAGNCNNTGNTTCCANAGAACN 3521
                                                                                                                                                                                                                                                                                                                                                      535 AGAAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGA 594
                                                                                                                                                                                                                                                                                                                                                                                                                               595 TAACGIGACCATGTATIGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAGACTT 654
                                                                                                                                                                                                 415 AUGITITIATCAAAACTCAGATTAAAGTGATTCCTGAATTTTCTGAACCAGAAGAGAAAT 474
                                                                                                                                                                                                                                                                              3522 TNANAAAGNANAGCCANAINTINAAICNICGAAANANANAITNAAAGGNAITGNINA 3578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                    Query Match
Best Local Similarity 45.5%; Pred. No. 0.12;
Matches 135; Conservative 0; Mismatches 161; Indels 1;
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-453-702B-14
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Search completed: September 3, 2004, 06:18:17 Job time : 85 secs

Page 1

BQ934226 AGENCOURT AY408392 Mus muscu BY704009 BY704009 BI456138 603172901	CR110248 CR13#065 G CR195636 AGBNCOURT B1694284 603347729 CB588736 AGBNCOURT CF41047 CR34065 G	CB587595 AGENCOURT CB512100 AGENCOURT CB587917 AGENCOURT B1454468 G03171428 BF182340 601804094 BG174435 G02334255	CD103859 AGENCOURT B124848 602992715 AV593197 AV593197 CD773806 AGENCOURT	BI694698 603347638 BI535437 398969 MA AW745952 urz4h02.y BT240806 60206571	CE440637 690932 MA BI304069 UI-R-DRO- AII2889 ga74602.X CR4407944 690549 MA	BX104255 BX104255 BF121576 601756977 BF439260 nab61h07. T12179 A533F Heart	BF123957 601758641 CB317710 AGENCOURT BX638501 BX638501 AI039039 0x30b10.s CB202990 AGENCOURT	BB75361 601230345 AI146280 qb87b10.x AV53196 AV593196 CF112025 Shultzomi AI112003 UI-R-YO-m	BF523627 UI-R-C1-1 BIS35434 398963 MA AIS02787 UI-R-C1-1 BF679243 602153429 CD572281 PBL 18 E0 BF150118 Uy82a09.y	AA23616 zs42109.s AW962400 EST374482 W97621 m697e12.r1 BY377460 BY377460 AW14807 EST291897 BR831558 BB8311558 BE28641 601094042 AA297231 EST112774 AI600132 EST251835 BY772480 BY772480	BY378738 BY378738 A1147044 qag82dd4.x BX517933 BX517933 BF148505 Uy882a09.x BY452021 BY452021 BU127029 603113730 AW240909 Uq38a03.x CB114632 K-EST0158 BY112564 BY112564	BY111994 BY111994 BY115292 BY115292 BV131955 603119028 BY789211 BY789211 BY086042 BY086042
828.6 69.2 926 1 826 69.0 954 2 708.8 59.2 1000 1 692.4 57.8 1011 1	674 56.4 800 1 674 55.3 961 1 668.4 55.8 961 1 650.6 54.4 845 1 623.8 52.1 803 1 623.	620.6 51.8 876 1 612.6 51.2 751 1 579.6 48.4 744 1 579 48.4 846 1 577 48.2 958 1	553.2 46.2 679 9 531.8 44.4 600 9 530.4 44.3 639 1	500.6 41.8 735 1 498.6 41.7 557 1 494 41.3 588 1 493.6 41.2 798 1	29 485.8 40.6 610 1.30 485.4 40.6 636 1.31 474.8 39.5 595 1.32 473 39.5 595 1.32	33 468 39.1 468 1.34 463.6 38.7 888 1.35 460 38.4 462 1.35 4.35 3.5 3.5 4.55 3.5 3.5 4.55 3.5 5.5 5.5 5.5 5.5 5.5 5.5 5.5 5.5	37 4419 35.5 856 1. 39 409.4 34.5 741 1. 40 385 32.2 399 9 41 379.8 31.7 1224 1.	42 3/8.6 31.6 733 10 44 371.6 31.0 468 9 45 369 30.8 433 10 46 366.9 30.6 487 9	24 356.2 30.5 504 10 49 358.8 30.1 404 17 50 358.4 29.9 882 10 51 352.2 29.4 509 14 52 356.4 29.3 407 10	54 332.6 27.8 391 55 329.6 27.8 416 57 327.6 27.4 416 57 319.2 26.7 44 58 312. 26.1 453 59 309.6 25.9 661 61 307 25.6 337 62 306.8 25.6 387	298.8 25.0 392 13 297.8 24.8 487 13 293.8 24.5 380 10 285 23.8 448 13 244 22.9 869 10 274 22.9 369 10 269.8 22.5 342 14 269.8 22.5 345 13	268.6 22.4 352 13 266.6 22.3 342 13 266 22.2 1109 13 263.4 22.0 338 13 261.6 21.9 341 13
5.1.6 Compugen Ltd.	8; Search time 2370 Seconds (without alignments) 15082.231 Million cell updates/sec	Caaaaaaaaaaaaaaa 1197	ω L	: 55026578	000	0 0	0 0		U C		1 by chance to have a the result being printed, ce distribution.	AK003748 Mus muscu AY408390 Homo sapi AY408891 Pom trogl AK014761 Mus muscu
GenCore version pyright (c) 1993 - 2004	nucleic search, using sw model September 3, 2004, 07:44:08; Se (withcast)	US-10-063-730-115 score: 1197 :: 1 cagcagtggtctctcagtccc table: IDENTITY_NUC Gapop 10-0 , Gapext 1.0	, s	iires Length Length	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries	EST:* 1: em_estba:* 2: em_esthum:* 3: em_estin:*	4: em_estmu:* 5: em_estov:* 6: em_estpl:* 7: em_estro:* 8: em_btr:*	9: gb_estl:* 10: gb_est2:* 11: gb_htc:* 12: gb_est3:* 13: gb_est4:*		20: em_gss_vrt:* 21: em_gss_vrt:* 22: em_gss_mus:* 24: em_gss_mus:* 25: em_gss_pro:* 26: em_gss_pro:* 26: em_gss_vri:* 27: em_gss_vri:* 29: gb_gss:*	the numbe than or by anal	965.8 80.7 1204 11 AK003748 954 79.7 954 29 AY408390 951.4 79.5 954 29 AY408391 949 79.3 1159 11 AK014761

REFERENCE  AUTHORS  TITLE  Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  JOURNAL  Nature 420, 563-573 (2002)  REFERENCE  Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Pukunishi,Y., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Pukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramco,N., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konoo,H., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,Y., Okaaaki,Y., Konio,H., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,Y., Okaaaki,Y., Salito,H., Salto,H., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shibata,Y., Shibata,Y., Shibata,Y., Shibata,Y., Shibata,Y., Shibata,Y., Shibata,Y., Yasunishi,P., Tanaka,T., Yoshida,K., Yoshino,M., Muramateu,M. and Hayashizaki,Y., Yoshida,K., Yoshino,M., Muramateu,M. and Hayashizaki,Y.,	<b>4</b> .	COMMENT Please visit our web Site (http://genome.gsc.iiven.go.jp// 10-1 further details.	prepared by using trendatose treatmoract.vacus, reversor and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence[5' adagaganganagancancancancantrantranarcancancccccccccc		/clone="1110017101" /tissue type="whole body" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="18-day embryo" misc_feature 86. 11037 /note="putative / note="putative / not	blasin, 95, match=1131, polyA_signal 11861191 fnote="putative" lolyA_site /note="putative"	Query Mat Best Loca Matches 1	
BY114233 BY114233 BU316501 603853392 BM487464 pgm2n.pk0 BU444969 603211494 BU444969 603211494 BU444969 603776782 AA028464 mi18003.r BU318544 603855369 BY114177 BY114177 BY376704 BY376704 AW258652 ug38603.y BY023640 BY023640 BU254396 603412791 AV009191 AV009191 CB319027 AGENCOURT BU404264 6041380137 BU405768 6041380137 BU405768 604138013	BB56945 BB369496 BB569496 BB369496 BB249867 603402144 BB090817 BB090817 BM491558 PGP2n.pk0	AK003748  Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110017101 product:tenomodulin, full insert sequence. AK003748	Craniata, Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.	A cloning ) u.N., Sugahara,Y., Shibata,K.,	Itch, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 11042159	<pre>Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Komo,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Chocda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okasaki, Y., Matshawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okasaki, Y., Matshawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okasaki, Y., Minishawa,T., Ozawa,K., Amanka, M., Amanka, M.,</pre>	risis (RISA) system 384-format llticapillary sequencer (2000)	on Research Group Phase II Team and the full-length mouse cDNA collection
78         258.4         21.6         329         13         BY114233           79         257.8         21.5         628         12         BM48466           80         257.6         21.5         628         12         BM484969           82         256         21.4         748         13         BU444969           82         25.3         21.2         34         3 BU44969           83         253.6         21.2         34         3 BU44969           84         253.6         21.2         34         3 BU44969           85         247.8         20.2         34         3 BU45973           86         247.8         20.7         320         13         BV11417           87         247.8         20.7         320         13         BV1417           87         247.8         20.2         34         13         BV25439           89         23         19.2         760         13         BV25439           90         22         19.0         34         BV3623           91         22         19.0         13         BV404264           93         14         CB19027	205.8 17.2 292 10 201.8 16.9 29 199.4 16.7 716 13 195 16.3 285 10 193.2 16.1 531 12	RESULT 1 AK003748 LOCUS DEFINITION Mus musculus 18-day embryo whole enriched library, clone:11100177 sequence. ACCESSION AK003748	AK003748.1 GI:12834607 HTC; CAP trapper. Mus musculus (house mouse) M Mus musculus (house mouse) Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;			AUTHORS Shibata, K., Itoh, M., Aizawa, K., Komno, H., Akiyama, J., Nishi, K., Sumi, N., Ishii, Y., Nakamura, S., Yamamoto, R., Matsumoto, H., Saka, Fujiwake, S., Inoue, K., Togawa, Y. Yoneda, Y., Ishikawa, T., Ozawa, K., Muzamatan M., Inone, K., Maramatan M., Inone, K., Inoue, K., Inou	TITLE RIKEN integrated sequence analy sequencing pipeline with 384 mu JOURNAL Genome Res. 10 (11), 1757-1771 MEDLINE 20530913 PUBMED 11076861 PREFERENCE 4	The RIKEN Genome Exploratic FANTOM Consortium. Functional annotation of a Nature 409, 685-690 (2001)

CCTCCAGAGAACTGTGAGGGCTGTCACATTCTAAATGCAGAAGCTCTGAAATCTAAGAAG 157

98

g ð 셤 ð 셤 ò qq à ΩD à g à q à d à d ð g ò DP ò g ð g à Пр

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GSS 12-DEC-2003
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, B., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAICCAAGAAAAIAIGIAAAICACIIAAGAIIIIGIGGACIGGIGIIIGGIAICCIGGCC 178
                                                                                                                                                      Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGTGCACGACTTTAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AY408390
Homo sapiens HCM3208 gene, VIRTUAL TRANSCRIPT, partial sequence,
                                                                                                                                                                                                                                                                                                                                              Clark.A.G., Glanowski.S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTAACTCTAATTGTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGGCAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGGCAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAATCCAAGAAATATGTAAATCCACTTAAGATTTGTGGACTGGTGTTTTGGTATCCTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CTAACTCTAATTGTCCTGTTTTGGGGGGGGCAAGCACTTCTGGCCGGAGGTACCCAAAAA
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/db_xref="taxon:9606"
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Location/Qualifiers
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AY408390.1 GI:39764361
                                                                        genomic survey sequence
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                                                                                                                             GAGCACACTITICTACAGCAATGGAGAAGAAGAATTTACATGGAAATTGATCCTGTG
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                GTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAAGCCTATGACATG
                                                                                                                                                                                                                                                                                398 TITAAAAATGGATACACTGGCATCTACTTTGTAGGTCTTCAAAAATGCTTTAATAAAACT
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                                                                79.5%; Score 951.4; DB 29 99.8%; Pred. No. 2.5e-172; iive 0; Mismatches 2;
/db_xref="taxon:9598"
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/locus_tag="HCM3208"
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1 (bases 1 to 954)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Givello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (16-7007-2003) Celera Genomics, 45 West Gude Drive,
Submitted (16-7007-2003) Selera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.

Location/Qualifiers
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                 AAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAAATTCTGGAGATTTGTGATAAC
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/wol_type="genomic DNA"
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Science 302 (5652), 1960-1963 (2003)
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/dev_stage="0 day neonate"
585._.992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 TCTACAGCAATGGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAGAACTG 320
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Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tenomodulin (MGD|MGI:1929885, GB|NM_022322, evidence:
BLASTN, 99%, match=1151)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TACTGAAGATTTGTGGACTAGTGTTTGGTATCCTGGCCTTAACTCTAATTGTTCTGTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGGAGCAAACACTTCTGGCCCGATGTATCCAAGATAACCTATGATATGGAGCACACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 CACTTAAGATTTGTGGACTGGTGTTTGGTATCCTGGCCCTAACTCTAATTGTCCTGTTTT
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Pred. No. 6.7e-172;
0; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="FANTOM_DB:4833424007"

/db_xref="MG1:1896631"

/db_xref="taxon:10090"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
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1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="putative"
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                                                            AK014761 1159 bp mRNA linear HTC 20-SEP-2003
Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched
library, clone:4833424007 product:tenomodulin, full insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, WRL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Buteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Group Phase I & III Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 1159)
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Adachi, J. Alzawa, K. Akahira, S., Akimura, T., Arai, A., Aono, H.,
Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
Hiraoka, T., Hori, F., Imotani, K., Ishi, T., Itoh, M., Izawa, M.,
Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
Salto, H., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K.,
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Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
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Direct Submission
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                          Mus musculus (house mouse)
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HTC; CAP trapper.
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Eukaryota; Metazoa;
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/dev stage="adult, 70 yr"
/dab_host="uplub"
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       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Gibrary Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LibAll3614 row: 1 column: 09
High quality sequence stop: 640.
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/db_xref="taxon:9606"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 926)

NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                 GATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAAACTCAGATTAAAG
                                                                 GATACACTGGCATCTACTTTGTAGGTCTTCAAAAATGCTTTATTAAAACTCAAATGCAAAG
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KEYWORDS
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QQ	481 AATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAATATCAGT 540	Matches	
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Š t	817 AGAATTTGATCCCATGCTGGATGAGAGGTTATTGTTGTTGATTTACTGCCGTCGAGGCAA 876	 	GCCTATGACATGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAATTTACATGGAA
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		oy Op	359 GAAGTGCACACTTTAAAAAGGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGT 418 
٥٧	992 CGC 994	, ,	TTATCAAAACTCAGATTAAAGTGATTCCTGAATTTTTCTGAAACTCAAAAAAAA
υþ	901 GGC 903		361 TITATTAAAACTCAAATCAAAGTGATTCCTGAATTTTCTGAACCAGAGGAAGAAATAGAT 420
RESULT 6		Q,	
AY408392 LOCUS	AY408392 954 bp DNA linear GSS 12-DEC-2003	Db 4	421 GAGAATGAAGAAATTACTACAACTTTCTTTGAACAGTCAGT
DEFINITION	le, VIRTUAL TRANSCRIPT, partial s	Å	539 AAGCCTATTGAAAACCGAGATTTTCTTAAAATTCCAAAATTCTGGAGATTTGTGATAAC 598
ACCESSION VERSION	AY408392 AY408392.1 GI:39764363	4 du	481 AAGCCTATTGAAAACAGAGACTTCCTGAAAATTCTAAAATTCTGGAGATTTGCGATAAT 540
SOURCE ORGANISM	Mus musculus (house mouse) Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria: Rodentia: Grinromath; Murian, Muria		
REFERENCE AUTHORS	1 (bases 1 to 954) Clark, A.G., Glanowski, S. Nielson D. Thomas D. Zeitzeller, Mullinde, Mus.		
	Todd, M.A., Tanenbaum, D.M., Titollo, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White T. T. Schinek, T. T.		
TITLE	Adams, M.D. and Cargill, M. Inferring nonneutral evolution from human-chimp-mouse orthologous	, 4 <u>c</u>	
JOURNAL	gene trios Science 302 (5652), 1960-1963 (2003)		CAAGAACTITICAATIBBBTGBCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
REFERENCE AUTHORS	130.1304 130.1308 1 to 954) Clark A.G. Glanowski s Mielen B mhomer 72.1		
	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheno, X. White T. T.	8 VQ	68
TITLE	Adams, M.D. and Cargill, M. Direct Submission	7 dū	
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	8 VO	
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment	·8 q <sub>Q</sub>	CATCTGT
FEATURES Source	Location/Qualifiers	λ <sub>0</sub>	
	/organism="Mus musculus" /mol_type="genomic DNA"	Op qu	
gene	/db_xref≈"taxon:10090" <1>954		
ORIGIN	/locus_tag="HCM3208"	BY704009	
Query Match Best Local	Query Match Best Local Similarity 91.6%; Pred. No. 2.6e-148;	ITION	1000 bp mRNA linear EST 16-DEC-2002 BY704009 RIKEN full-length enriched, 18-day embryo whole body Mus musculus cDNA clone 1110017101 5', mRNA sequence.
			BY /04009

linear EST 16-DEC-2002
-day embryo whole body Mus sequence. .TGCTGGGGAGGTCTAA 1012 ||||| ||||| |||||| |TGCTTGGGAGGTCTAA 954 BY704009 ACCESSION

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FEATURES
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Nikaldo, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9225
Fax: 81-45-503-9216
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URL:http://genome.gsc.riken.go.jp,

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Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Taqami, M.,

Direct Submission

Computational Analysis of Full-Length Mouse CDNAS, Compared with
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (200)
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                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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GI:27115128
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                                                                                                     Mus musculus
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/tissue_type="whole body"
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1 (bases 1 to 800)
Yi,Y., Desai,R., Olarte,M., Henthorn,P. and George A.L.
                                                                 CACTICIGGCCCGAGGIATCCAAGAAACCIATGACATGGAGCACACTITCTACAGCAAC
                                                                                                                             CACTICIGGCCGGAGGIACCCAAAAAGCCIAIGACAIGGAGCACACTITCIACAGCAAI
                                                                                                        GGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCCAGAACTGAAATATTCAGA
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                                                                                                                                                                             AGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAACGGATACACTGGC
                                                                                                                                                                                                                                                  ATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAAACTCAGATTAAAGTGATTCCTGAA
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MNH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TGTCACATICTAAATGCAGAAGCTCTGAAATCTAAGAAGATATGTAAATGCACTGAAGATT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cloud lib="NCI CGAP Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
Site 2: Not1; Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAAATATGTAAATCACTTAAGATT 151
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                                                                            GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATG
                                                                                                              GCTATACACATA---CCCTACTGCTACAAAGGNGGTNGAGTC-TCTGTCGTGTCATCATG
         TGTTGTATTTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTA
                                          --GITGITITACIGICGICGAG--AAACCGIACIGCGCCG-GICTGIGAGNITITACIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enail: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov a column: 02
Plate: LiAMILG37 row: a column: 02
High quality sequence stop: 810.
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/clone="IMAGE:525233"
/clssue_Yppe="tumor, gross tissue"
/dev stage="7" months"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 692.4; DB 12;
Pred. No. 9.6e-123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 136;
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/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                     (house mouse)
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Best Local Similarity 85.3%;
Matches 856; Conservative
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FEATURES

ORIGIN

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by, David Rowe. Library constructed by ResGen, Invitrogen Corp."
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. David Rowe

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM0038 row: e column: 14

High quality sequence stop: 662.
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       TGGAGATTTGTGATAACGTGACCATGTATTGGATCAATCCCCACTCTAATATCAGTTTCTG
                            AGTTACAAGACTTTGAGGAGGAGGAGAAGATCTTCACTTTCCTGCCAACGAAAAAAA
                                                                                                                 639 AGTIACAAGACTITICAGGAAGATGGTGAAGATCTICACTTICCTACCAATGAAAAAAA
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AGENCOURT 11259532 NIH MGC_135 Mus musculus cDNA clone
IMAGE:30137293 5', mRNA sequence.
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89.4%; Pred. No. 3.3e-119;
iive 0; Mismatches 86;
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Best Local Similarity 89.4%;
Matches 748; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98
                                                                  Division of Genetic Medicine
Division of Genetic Medicine
Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, 1781: 615 936 266
TRAIN 1615 936 266
Email: al-george@vanderbilt.edu
Insert Length: 1647 Std Error: 0.00
Seq primer: T7: TAATACGACTACTATAGGG
High quality sequence start: 39
High quality sequence stop: 797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 TAAATGCAGAAGCTTTTAAATCCAAGAAGATATGTAAATGACTTAAGATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAAGATTTACATGGAAATTGATCCTGTGACCAGAACTGAAATATTCAGAAGCGGAAATG
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                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="heart"
/dev stage="mixed developmental stages (adult, 30 day
day Fetal)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Canine heart normalized cDNA Library in pBluescript"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 14; Length 800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47; Indels
Expressed sequence tags from Canine heart Unpublished (2003)
Other_ESTs: CH3#065_G01T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 56.4%; Score 674.8; DB 14 Best Local Similarity 93.7%; Pred. No. 2.4e-119; Matches 714; Conservative 0; Mismatches 47;
                                                                                                                                                                                                                                                                                              'organism="Canis familiaris"
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/db_xref="taxon:9615"
                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9615'
/clone="CH3#065_G01"
                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="heart"
                                                            Contact: George AL
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89.5%; Pred. No. 3.9e-118;
.ive 0; Mismatches 86; Indels
                                                                                                                                                                                              sample"
          Library Arrayed by: The I.M.A.G.E.
                                                                                                                                      mol_type="mRNA"

%stain="FVBN-3"

db xref="taxon:10090"

clone="IMAGE:5375335"

tissue type="tumor, biopsy sc

dev stage="5" months"

lab_nost="DH108"
                                                                                                                                                                                                                                 /clone_lib="NCI_CGAP_Mam2"
                                                                                                                             organism="Mus musculus"
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603347729F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5375335 5',
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NH-WGC http://mgc.ncl.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
CCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA
                   ATATGTAAATCACTTAAGATTTGTGGACTGGTGTTTGGTATCCTGGCCCTAACTCTAATT
                                                                     GTCCTGTTTTGGGGGGGGGCACTTCTGGCCGGAGGTACCCAAAAAAGCCTATGACATG
                                                                                                                             GTCCTGTTTTGGGGGAGCAAACACTTCTGGCCCGAGGTATCCAAGAAAACCTATGACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
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4 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall; Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" 419 479 280 340 599 719 629 779 580 839 640 899 700 be TTGATCCTGTGACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGG CCTATGACATGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAA AAGTGCACGACTTTAAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTT TTATCAAAACTCAGATTAAAGTGATTCCTGAATTTTTCTGAACCAGAAGAAGAATAGATG 540 AGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATAACG TGACCATGTATTGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGG AGGAGGGAGAAGATCTTCCTTCCTGCCAACGAAAAAAAAGGGATTGAACAAAATGAAC AAGAACTICCAATAAATGACTATACTGAAAATGGAATAGAATTTGATCCCATGCTGGATG AGAGAGGTATTGTTGTTATTTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCGTCTGTG 641 AGAGAGTIACTGTTGTATTTACTGTCGAGGCAACCGTTACTGCCGCCGTGTCTGTG Gaps DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lfound through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAMI1955 row: j column: 08
High quality sequence stop: 892.
Location/Qualifiers

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CF410247
CH3#065_G01T3 Canine heart normalized cDNA Library in pBluescript Canis familiaris cDNA clone CH3#065_G01 3', mRNA sequence.
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Division of Generalty
Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
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                     <u>CAGAGGAAGAATAGATGAAGAATTACTACAACTTTCTTTGAACAGTGA</u>
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut.
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Can
1 (bases 1 to 80)
Yi,Y., Desai,R., Olaste,M., Henthorn,P. and George A.L.
Expressed sequence tags from Canine heart
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Other_ESTs: CH3#065_G01T7
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Canis familiaris
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
Thissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencout Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: NDAM31 rowe; j column: 04
High quality sequence stop: 738.
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             GTGTCATCATGCCTTGTAACTGGT-GGGTGGCCCGCATGC-TGGGGAGGGTCTAATAGG-
                                                                                                            GIGICATCATGCCTTGCAACTGGGGTGGGCCCGCATGCTTGGGAAGAGTCTAATAGGC
                                                                                                                                                    AGGITIGAGCICAAAIGCIIAAACIGCIGGCA-ACAIAIAAIAAAIGCAIGCIAIICAAI
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                                                                                                                                                                                                                                                                                                                                                      CB588736
AGENCOURT 12567644 NIH MGC_136 Mus musculus cDNA clone IMAGE:30290619 5', mRNA sequence.
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Query Match Best Local Simi Matches 712;

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Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                               foreselorgan: heart; Vector: pBluescript; Site 1: 5' of vector Not1; Site 2: 3' of vector EcoR; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 629 ATATCAGITICTGAGITACAAGACITIGAGGAGGAGAGAGAAGAICTICACITICCTGCC 688
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                                                                                                                                                                                                                                          /tissue_type="heart"
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day_fetal)"
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                                                                                                                                                                                                                                                                                                           /clone_lib="Canine heart normalized cDNA Library in pBluescript"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.1%; Score 623.8; DB 14;
llarity 91.1%; Pred. No. 1.4e-109;
Conservative 0; Mismatches 63;
Tel: 615 936 2660
Fax: 615 936 2661
Email: al.george@vanderbilt.edu
Insert Length: 1647 Std Error: 0.00
Seq primer: T3: ATTAACCTCTAAAAGGGA
High quality sequence start: 69
High quality sequence stop: 741.
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/mol_type="mRNA"
/db_xref="taxon:9615"
/clone="CH3#065_G01"
                                                                                                                               Location/Qualifiers
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Best Local Similarity
Matches 674; Conserv
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Nkaido,I., Coato,N., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schrimi,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaaterland,T. Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincoch,S., Hirokawa,N., Jackson,I.J., Jarvis,B.D., Kanai,A., Kawasawa,Y., Kedierski,R.M., King,B.L., Konagaya,A., Kavaij,H., Kawasawa,Y., Kedierski,R.M., King,B.L., Marchonni,L., McKenzie,L., Miti,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Sandelin,A., Schou,M.S., Stou,M.S., Stou,M., Shinada,K., Sandelin,A., Schou,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wanner,L., Wahlestedt,C., Wanny,Y., Watanabe,Y., Walls,C., Wilming,L.G., Wynshaw,Woris, Sandelin,R., Zavodan,M., Zhu,Y., Zimmer,A., Hashizume,R., Yasunishi,Y., Kawa,T., Kagawa,I., Miyazaki,A., Hashizume,W., Imotani,K., Itoh,M., Kagawa,I., Miyazaki,A., Hashizume,W., Imotani,K., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Ysunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E., and Hayashizaki,Y., Rhallysis of the mouse transcriptome based on functional annotation of 60,770 cull-length cDNAs
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203 CAAACATATAATAAATGCATGCTATCCAATGAATTTCTGCCTATGAGGCATTTGGTTCCT 144
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

    (bases 1 to 932)

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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bmail: genome_rese@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Badchi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itchi,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
                                                                                           1106 GGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTT
                                                                                                                                                              143 AGTAGCCAGTACTCCAGAATTACTTGTAGGTAATTCCTCTCTTCTTCTATCTTAATAAACTT
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Sciurognathi; Muridae; Murinae; Mus.
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       ATTCAGAAGCGGAAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAACGGATA
                                                 ATTCAGAAGTGGGAAATGGCACTGATGAAACATTGGAAGTCCATGACTTTTAAAATGGATA
                                                                                                CACTGGCATCTACCTTCGTGGGTCTTCAAAATGTTTTATCAAA-ACTCAGATTAAAGTGA
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
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Mammalia; Butheria; Rodentia;
1 (bases 1 to 876)
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TITLE
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CB587595
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequence din Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 cagcaacgecgagaagaagartracarggaarirgarccaraaccagaacagaar 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GAAGATTIGIGGACTAGIGITIGGIATCCIGGCCTTAACTCTAATTGTTCTGTTTTIGGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAAATATGTAAATCACT 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGCAATGGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAGAACTGAAAT 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŗ.
Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Site 1: Sal1; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGAGCACACTTTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAGCAAGGAAAGATACTGTGTGCTGAGAGCCATGGCAAAGAATCCTCCAGAGAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAAGCTGGGAAAAGAGCACCGTGTGCTGGGAGACCATGGCAAAGATTCCTCCAGAGAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 TAAGATTTGTGGACTGGTGTTTGGTATCCTGGCCCTAACTCTAATTGTCCTGTTTTGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'clone_lib="RIKEN full-length enriched, 0 day neonate
                                                                                                                                                                                                                                                                                                                                              prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.0%; Score 623; DB 13; Length 932; llarity 83.9%; Pred. No. 1.9e-109; Conservative 0; Mismatches 137; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rissue type="head"
dev stage="0 day neonate"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="4833424007"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                           details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 726; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85
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Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH
Bldg: 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Produremnt: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Biscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LIML at:
Plate: NDCM195 row: n column: 02
High quality sequence stop: 553.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab host="NHIOB (T1 phage-resistant)"
/clone_lib="NIH_MGC 186"
/clone_lobgan: Pooled-Skin; Vector: pDNR-LIB; Site 1: Sfil
(ggccattatggc); Site 2: Sfil (ggccgcctcggc); Library is
oligo-dr primed and directionally cloned. cDNA was
prepared from a pooled samples of tissues from Skin,
                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Buteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGCCTATGACATGGAGCACACTTTCTACAGCAATGGAGGAAGAAGAAGAAGATTTACATGG 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTTATCAAARCTCAGATTAAAGTGATTCCTGAATTTTCTGAAACCAGAAGAGAAATAG 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             meninges, duramatter, pia matter and choroid pleaus. 5, and 3, adaptors were used in cloning as follows: 5, adaptor sequence: 5'-CACGCCATTANGCC3' and 3' adaptor sequence: 5'-CACGCCATACCGACAGCCCACAGCATG-dT(30) BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech inboratories (Palo Alto, CA). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 AAGCCTATGACATGGAGCACACTTTCTACAGCAATGGAGAAGAAGAAGAAGATTTACATGG
                                                                                                                                                                                                                                                                                                                                                              NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGAAGTACACGACTTTAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAAT
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                                                                                        CD512100
AGENCOURT 14354032 NIH MGC 186 Homo sapiens cDNA clone IMAGE:30406681 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.2%; Score 612.6; DB 14; Length 751; 99.2%; Pred. No. 2e-107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2e-107;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30406681"
                                                                                                                                                                                        GI:31443818
                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                            (bases 1 to 751)
                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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Best Local Similarity 99.2°
Matches 626; Conservative
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                                                                                                                                                                                                                                                                     Homo sapiens
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CD512100.1
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                                                                                                            DEFINITION
                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                           ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
JOURNAL
                                    RESULT 16
CD512100
                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                            KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
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                                    /tissue type="embryonic limb, maxilla and mandible"
/lab_host="lab" (phage-resistant)"
/clone lib="WHH MGC 136"
/clone lib="WHH MGC 136"
/note="Wector: pGWV-SPORT6.1; Site 1: ECGRV; Site 2: NotI;
Normalized, full-length enriched library from pool of mouse embronic limb, maxilla and mandible, embryonic day
17.5, 18.5 and newborn (mandible (5, 4 and 1 limb and jaw equivalents from respective days). Cloned directionally, oligo-dT primed (5'-GACTAGTTCTAGATCGCGAGCGGCCC(T)15-3.
Size selected for the >1kb fragments, average insert size
1.2 kb. Normalization to Cot 7.5 Tissue contributed by David Rowe; library constructed by ResGen, Invitrogen
Corp. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 ATATGTAAATCACTTAAGATTTGTGGACTGGTTTTGGTATCCTGGCCCTAACTCTAATT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACCGAGATTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTAT 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACAGAGACTTCCTGAAAATTCTAAAATTCTGGAGATTTGCGATAATGTGACCATGTAC 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGAGAAA 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                redarchariccaricraarageagriricagaarracagacririgageagaacacreaa 675
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTAAAAACGGATACACTGGCATCTTCGTGGGTCTTCAAAAATGTTTTATCAAAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 14; Length 876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 620.6; DB 14;
Pred. No. 5.7e-109;
0; Mismatches 79;
/db_xref="taxon:10090"
/clone="IMAGE:30295278"
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 89.4%;
Matches 680; Conservative
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Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musina
Size selected for the >1kb fragments, average insert size 1.2 kb. Normalization to Cot 7.5 . Tissue contributed by David Rowe, library constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."
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                                                                                                                                                   50.8%; Score 608.2; DB 14, 91.1%; Pred. No. 1.3e-106; iive 0; Mismatches 63;
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Matches 646; Conservative
                                                                                                                                                             Query Match
Best Local Similarity
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// Ab xref="mRNA"
/ Ab xref="mRNA"
/ Clone="IMAGE:30292458"
/ Clone="IMAGE:30292458"
/ Lissue type="embryonic limb, maxilla and mandible"
/ Lab host="DH10B (phage-resistant)"
/ Clone="Lib="mNH MGC-136"
/ Anote="Wector: pGMV-SPORT6.1; Site 1: BCoRV; Site 2: NotI;
/ Normalized, full-length enriched library from pool of mouse embronic limb, maxilla and mandible, embryonic day
17.5, 18.5 and newborn (mandible (5, 4 and 1 limb and jaw equivalents from respective days). Cloned directionally, oligo-dT primed (5'-GACTAGTTCTAGATCGCGAGGGCGCCC(T)15-3'.
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                 234 GITITAICAAAACICAGAITAAAGIGATICCIGAAITITICIGAACCAGAAGAGAAAIAG
                                                                   AAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATA
                                                                                                                                                                                                                                                              ACGIGACCATGIATIGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAGACTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapDs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information clone distribution: MGC clone distribution information can k
http://mage.llnl.gov
Plate: NDAM316 row: f column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CBS87917
AGENCOURT 12990010 NIH MGC 136 Mus musculus cDNA clone IMAGE:30292458 5', mRNA sequence.
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VERSION
KEYWORDS
SOURCE
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TITLE
JOURNAL
COMMENT
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CB587917
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gross tissue"
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Pred. No. 5.3e-101;
0; Mismatches 85;
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/organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="tumor, g
/dev_stage="7 months"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                 BF182340.1 GI:11060482
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SOURCE
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                                                                                                                                                                                                                                                                                       DEFINITION
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VERSION
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AUTHORS
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                                                 Email: cgapbs-remail.nin.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.lln.gov
Plate: LiAM11633 row: h column: 08
High quality sequence start: 2
High quality sequence start: 2
High quality sequence stop: 733.
Location/Qualifiers
Lirea I.T.744
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/clome_lobe".
//clome_lobe".
//clogan: mammary: Vector: pCMV-SPORT6; Site 1: SalI;
//clomed unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigators
Library constructed by Life Technologies. Investigators
NIP" Annighausen/Robin Humphreys,
NIH"
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 National Institutes of Health, Mammalian Gene Collection (MGC)
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/dev_stage="7 months"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 579.6; DB 12
Pred. No. 4.2e-101
                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="C57BL/67"
/db_xref="taxon:10090"
/clone="IMAGE:5250871"
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Best Local Similarity 90.7%;
Matches 640; Conservative
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                                                                                                                                                                                                                             TIGGAICAAICCCACICIAA-IAICAGIITICIGAGITACAAGACIITIGAGGAGGAGGAG
                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Perparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9308 row: & column: 23
High quality sequence stop: 703.
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/note="Organ: mammary; Vector: pCWV-SPORT6; Site 1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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GTCCTGTTTTGGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAAGCCTATGACATG

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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. Bukaryota; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 558)

S NIH-MGC http://mgc.nci.nih.gov/.

In Thoublished (1999)

LOUDACH: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CONDA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CLONA Library Preparation: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at: http://image.llh.gov

Plate: LLAM10254 row: m column: 13
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                                                                                                                                                                                                                                                          CAGATTAAAGTGATTCCTGAATTTTCTGAACCAGAAGAAGAAATAGATGAGAATGAAGAA 490
                                                         ACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGAC 370
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                                                                                                                                   491 ATTACCACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAA
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Greergritingggggaggaacacriterggecegaggartecaagaaaaccrargacarg
                                      GAGCACACTITICTACAGCAATGCAGAGAAGAAGAATTTACATGGAAATTGATCCTGTG
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/mol_type="mRNA"
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High quality sequence stop: 652.
Location/Qualifiers
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Mus musculus
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/gtrain="FVB/N"
/db xref="taxon:10090"
/clone="Index:4457652"
/tissue type="tumor, biopsy sample"
/tissue type="tumor, biopsy sample"
/dev stage="10 months, virgin"
/lab_hogt="DH108"
/clone lib="NCI CGAP Mam1"
/clone lib="NCI CGAP Mam1"
/note="Organ: mammary; Vector: pcMV-SPORT6; Site 1: Sal1;
Site 2: Not1; Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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                                                                                                                                                                                                                                                41 ACTGTGTGCTGAGAGACCATGGCAAAGAATCCTCCAGAGAATTGTGAAAGACTGTCACATT
                                                                                                                                                                                                                                                                                                         101 CIAAAIGCAGAAGCIITITAAAICCAAGAAAATAIGTAAAICACITAAAGAITIGIGGACIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 AAGAAGATTTACATGGAAATTGATCCCATAACCAGAAACAGAAATATTCAGAAGTGGAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD103859 712 bp mRNA linear ES:
AGENCOURT 14008022 NIH_MGC_186 Homo sapiens cDNA clone
IMAGE:30372251 5', mRNA sequence.
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                                                                                                                                                                           48.2%; Score 577; DB 12; ilarity 89.3%; Pred. No. 1.2e-100; Conservative 0; Mismatching
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CD103859.1 GI:30757033
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                                                                                                                                                                                                                            Matches 633;
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CD103859
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BI248748 679 bp mRNA linear EST 17-JUL-2001 602927715F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5148842 5',
                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCNV-SPORT6; Site_1: Sal1;
Site_2: NotI; Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
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                                                                                                                                                   777 AGGAAGAACTICCAATAAATGACTATACTGAAAA--TGGAATAGAATTTGATCCCA 830
                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Bmail: GapbS-r@mail.nh.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 679)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11367 row: m column: 03
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High quality sequence stop: 677.
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/clone="IMAGE:5148842"
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/lab_host="DH108"
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/strain="C57BL/6J"
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BI248748.1 GI:14795446
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ilarity 91.7%;
Conservative (
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Best Local 8
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ORGANISM
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BI248748
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                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLOWIECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: NDCM164 row: c column: 12
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                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 712)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 AGGCCTATGACATGGAGCACACTTTCTACAGCAATGGAGAAGAAGAAGAAGATTTACATGG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGAAGIGCACGACTTTAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAT 416
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                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 712;
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Query Match

Best Local Similarity 98.8%; Pred. No. 5.1e-100;

Matches 589; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 494.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30372251"
                                      Homo sapiens
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NIH-WGC http://mgc.nci.nih.gov/, NIH-WGC http://mgc.nci.nih.gov/, National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Bos taurus"
/organism="Bos taurus"
/mo__type="mRNA"
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/clone="pto-conf6A12"
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/lab_host="DH108"
/clone lib="Bos taurus cartilage fetus"
/clone lib="Bos taurus cartilage fetus"
/note="Vector: pZL1; Site_1: Sal1; Site_2: Not was deleted from a Not1 site"
                                                                                                                                                                                                                                  600;
                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                    37; Indels
                                                                                                                                                                                                                                44.4%; Score 531.8; DB 9; ilarity 93.7%; Pred. No. 6.5e-92; Conservative 0; Mismatches 37;
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Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000
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                              GTCCTGTTTT-GGGGAGCAACACTTCTGGCCCGAGGTATCCAAGAAAACCTATGACATG 256
       ATATGTAAATCACTTAAGATTTGTGGAGTGGTGTTTGGTATCCTGGCCCTAACTCTAATT 190
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                                                                                 GICCIGITITGGGGGGGGGCACTICTGGCCGGAGGTACCCAAAAAGCCTATGACATG
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Animal Genetics Division
Shirawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Jape
11 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
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ACCESSION VERSION KEYWORDS SOURCE

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COMMENT

FEATURES

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BI694698 735 bp mRNA linear EST 18-SEP-2001
603347638F1 NCI_CGAP_Mam2 Mus musculus cDNA clone IMAGE:5375361 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363 IGCACGACITIAAAAACGGAIACACIGGCAICIACIICGIGGGICTICAAAAAIGITITA 422
                                                                                                                                                                              546 CTTCCTGAAAATTCTGGAGATTTGCGATAAATGTGACCATGTACTGGATCAAT
                      TTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
http://mage.llnl.gov
High quality sequence start: 8
High quality sequence stop: 732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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88.7%; Pred. No. 5.7e-86;
Live 0; Mismatches 69; Indels 9;
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/dev_stage="5 months"
/lab_host="DH108"
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/mol_type="mRNA"
/strain="FVB/N-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                         644
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/clone="IMAGE:5375361"
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"

/mol_type="mRNA"
//mol_type="mRNA"
//db_xref="rexxon:10090"
//clone="ImAGE:305064556"
//lab_host="DH10B (phage-resistant)"
//clone="Dragn: Pooled" - Molar; Vector: pDNR-LIB; Site_1:
Sfil (ggccattatggcc); Site_2: Sfil (ggccgctcggcc);
Non-normalized full-length enriched library 5' and 3'
adaptors were used in Cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTACAGGCGCATATGGCC-3' and 3' adaptor sequence:
5'-ATTCTACAGGCGGACGACATG-dT(30)BN-3' (Where B = A,
C, or G and M = A, C, G, or T). Average insert size 1.71
kb (range 0.5-3.0 kb). 15/15 colonies contained inserts by
PCR. This library was enriched for full-length clones and
was constructed by Clontech Laboratories (Palo Alto, CA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ۲;
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                      Contact: Daniela S. Gerhard, Ph.D.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH

BldG. 31 RmlOA07 Bethesda MD 20892

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Yoshihiko Yamada, Takashi Nakamura, NIDCR

CDNA Library Preparation: CLONTECH Laboratories, Inc.

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be http://image.llnl.gov
Plate: NDCM292 row: d column: 05

High quality sequence stop: 529.
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                                                                                                                                                                                               Takashi Nakamura, NIDCR
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44.3%; Score 530.4; DB 14; Length 639;
Best Local Similarity 91.5%; Pred. No. 1.2e-91;
Matches 572; Conservative 0; Mismatches 52; Indels 1;
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AW743952 588 bp mRNA linear EST 27-APR-2000 ur24h02.yl Soares mouse NMBP Mus musculus cDNA clone IMAGE:3025299 5' similar to TR:Q9Y163_Q9Y163 CHONDROWODULIN-I PRECURSOR. ;, mRNA
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 588)
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                                                                                                                                                    /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from day 20 and day 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     305 rearcecarraccaaaacreaaararreacaagregaaaregecacreargaaacarrega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 AGTGCACGACTITAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTT
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                                                                                                                                                                                                                                           41.7%; Score 498.6; DB 12; Length 93.9%; Pred. No. 1.5e-85; ative 0; Mismatches 34; Indels
                                                                    /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab host="DH10B"
/clone_lib="MARC 4BOV"
                                                    /organism="Bos taurus"
Seq primer: ATTIAGGTGACACTATAG
              Location/Qualifiers
1. .557
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Bos taurus
Busaryotas, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Lagreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Guackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                      406
                                                                                                                                                                                                                                                                                                                                                                  778
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Single pass sequencing. Bases called and alt trimmed with phred
Vo.980904.e. Vector identified by cross_match with the -minscore
and -minmatch 12 options.
PCR PRimers
                                                                                                                                                  602
                                                                                                                                                                                                                         662
                           ALGAAGAAATTACTACAACTITCTTTGAACAGTCAGTGATTTGGGTTCCCGCAGAAAGC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGAGAGAGGTTATTGTATTTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCCGTCTG
                                                                                                                                                                                    CTATTGAAAACAGAGACTTCCTGAAAATTCTAAAATTCTGGAGATTGCGATAATGTGA
                                                                                                                                                                                                                                                                                            AGGGAGAAGATCTTCGTTTCCTGCCAACGAAAAAAAAAGGGATTGAACAA--AATGAACA
                                                                                                                                                                                                                                                                                                                                                                                            GAAGAACITCCAATAAATGACTATACTGAAAAT-GGAATAGAATTTGATCCCATGCTGGA
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         TCAAAACTCAGATTAAAGTGATTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGA
                                                                            AIGAAGAAATTACCACAACTTTCTTGAACAGTCAGTGATTGGGTCCCAGCAGAAAGC
                                                                                                                                                  CTATTGAAAACCGAGATTTTTCTTAAAATTCCAAAATTCTGGAGATTTGTGATAACGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         557 bp mRNA linear 198959 MARC 4BOV Bos taurus cDNA 5', mRNA sequence. B1535437.1 GI:15376545 BST.
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PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      898 TGAACCTTTACTAGGCTACTACCCATATC 926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         706 TGAACCTTTACTAGGCTACTACCATACC 734
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BACKWARD: GTTTTCCCAGTCACGACG
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Contact: Smith TPL
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Fax: 402 762 4390
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602995241F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5150867 5',
                                                                                                                                                                                                                                                  /clone_lib="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCNV-SPORT6; Site 1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: \(\tilde{0}\) iso dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      311 ACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGAC 370
                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Iissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMI1373 row: a column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 crcrcacrcrcaaadcacdcaaaadacaccargracradagacaccardaadaar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 493.6; DB 12; Length 798;
Pred. No. 1.2e-84;
0; Mismatches 49; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH108"
              555 GACCAGAATGAGCAATGGGTGGTCCCGCAAGTGA 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 796.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTACCCAAAAAAAGCCTATGACATGGAGCACACTTTCTACAGCAATGGAGAGAAGAAG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   287 AITTACATGGAAATTGATCCTGTGACCAGAACTGAAATATTCAGAAGCGGAAATGGCACT 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                     Tumor Gene Index (1997)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 GGTATCCTGGCCTTAACTCTAATTGTCCTGTTTTGGGGGAGCAACACTTCTGGCCCGAG
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Pred. No. 1.1e-84;
0; Mismatches 50; Indels
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                                                                                                                                                          Seq primer: -40RP from Gibco
High quality sequence stop: 486.
Location/Qualifiers
1. 588 /organism="Mus musculus"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.3%;
91.3%;
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Best Local Similarity 91.3
Matches 524; Conservative
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                                                                                                                                          TGAACAGTGGGTGCTCCTCAAGTGAAGTAGAGAAGACCCGTCACGCCAGACA---AGC
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                            TAACGTGACCATGTATTGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAGACTT
                                                                                               Genome Res. 6 (9), 791-806 (1996)
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Rattus norvegicus
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Fax: 319 335 9565
Email harm
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Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G.,
Wray, J.E. and Keele, J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PDD Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                                                                                                                                                  490
                                                                                                                                                                                                                                                                                                  659 ATTACTACAACTTTCTTTGAAACAGTCAGTGATTGGGTTCCCCGCAGAAAAAGCCTATTG 718
                                                                                                                                                                                                                                                                                                                                                  607
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/tissue_type="pooled"
/tisb host="DH10B"
/clone_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
/incle="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
/incleding liver: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
//oce="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
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ritaaaaarggatacacregcarcracrirgraggicricaaaargcritarraaaacr
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Pred. No. 4.1e-83;
0; Mismatches 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9913"
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CB440637.1 GI:29226859
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90.2%;
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Matches 544; Conserv
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CB440637
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636 bp mRNA linear EST 20-JUL-2001
UI-R-DR0-cjc-o-14-0-UI.S1 UI-R-DR0 Rattus norvegicus cDNA clone
UI-R-DR0-cjc-o-14-0-UI 3', mRNA sequence
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Dence Soares@ulowa.edu

The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 636)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 5224;
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/ulganian=_nacture_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not_served_not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTTAAACTGCT----GGCAACATATAATAATGCATGCTATTCAATGAATTTCTGCCTA 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1089 TGAGGCATCTGGCCCCTGGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATTCCTCTTT 1148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGAGAAGA 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277
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and the oligo-dr track served to verify it as a clone from the non-normalized osteoblast library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 636 CAGAGACTICCIGAAAATICIAAAATICIGGAGATITGCGACAATGIGACTATGIACIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 485.4; DB 1
Pred. No. 4.9e-83;

    636
    organism="Rattus norvegicus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAG_TISSUE=osteoblast
TAG_LIB=UI-R-DR0
TAG_SEQ=AAGATATCAA"
                                                                                                                                                                                                                                     location/Qualifiers
                                                                                                                                                       Seg primer: M13 Forward POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40.6%;
87.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 87.0°
Matches 561, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   673
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qa74e02.x1 Soares fetal heart NbHH19W Homo sapiens cDNA clone IMAGE:1692506 3' Similar to SW:CHM1_BOVIN P17404 CHONDROMODULIN-I PRECURSOR;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420
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                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 591 Std Error: 0.00
Seq primer: -40m13 fwd. Er from Amersham
High quality sequence stop: 440.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     759 ACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTGAAAATGGAATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               819 AATTIGATCCCAIGCIGGAIGAGAGGGITATIGITGIATTIACTGCCGICGAGGCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           699 AAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479 AAGGGATTGAACAAAATGAACAGTGGTGGTCCCTCAAGTGAAAGTAGAAGAAGACCCGTC
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                   Score 474.8; DB 9;
Pred. No. 5.7e-81;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="IMAGE:1692506"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapier
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="unknown"
                                                                                                                                                                           AI123839.1 GI:3539605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.7%;
                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                              Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ".WbHL19W."
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Best Local Similarity 99.6
Matches 476; Conservative
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                                                                                                  LOCUS
                                                                      RESULT 31
AI123839/c
                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                            ACCESSION
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KEYWORDS
                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                          JOURNAL
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468 bp mRNA linear EST 06-FEB-2003
BXIO4255 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
IMAGP980034297 ; IMAGE:1692506, mRNA sequence.
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                                                                                                                                                                                                                                                                                                         GTCATCTGTCGTGTCATCATGCCTTGTAACTGGTGGGCCCGCGTAGCTGGGGAGGGTC 1009
                                                              770 GCAAGTGAGGAAGAACTTCCAATAAATGACTATACTGAAAATGGAATAGAATTTGATCCC 829
                                                                                            889
                                                                                                                                                                                        296
                                                                                                                                                                                                                              949
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26
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neubert, P., Partsch, E., Peters, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1066 GCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCTCTCCAGAAT
                                                                                                                                                830 AIGCIGGAIGAGAGGITATIGITGTAITTACTGCCGTCGAGGCAACCGCTAITGCCGC
                                                                                                                                                                                      355 Argricdardadadarracrerrerarrizacrecerceaceaaceeracee
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                                                                                                                                                                                                                                                                                                                                                                                         1010 TAATAGGAGGITTTGAGCTCAAATGCTTAAACTGCTGG----CAACATATAAATGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 TGCTTGTAGGTAATTCTTCTCTTCATGTTCTAATAAATTTCTACACCCTCAAAAA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RZPDILIB: I.W. AG E. CDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDILB No.972)
http://www.rzpd.de/CloneCards/cg1.
bin/showLib.pl.cgi/response7libNo=972
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ebert, D., Heil, O., Hennig, S., Neubert, P., Partsch, B., Pete Radelof, U., Schneider, D. and Korn, B.

Human UnigeneSet - RZPD3
Unpublished (2003)
Contact: Ina Roseourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
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/mol_type="mRNA"
/mol_txpe="mRNA"
/db_xref="t=xon:9606"
/clone="IMAG99980034297; IMAGE:1692506"
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/dev_stage="19 weeks"
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Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: FOY8047 row: F column: 8
Seq primer: TAGAAGGCACAGTCGAGG.
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                                                                                                                                                                                                     AATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCTCT 1118
                                                                                                                       TGGGGAGGGTCTAATAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATATAATA 1058
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1 (bases 1 to 595)
Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.
                                                                       resecadescriatascarestricaecteaariscriaaacrectectacaacarataara 120
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/lab host="DHIOB"
/clone_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
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/db_xref="taxon:9913"
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MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/lab_host="DH10B (ampicillin resistant)"
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0
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100.0%; Pred. No. 1.2e-79;
iive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 468; Conservative
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ð qq à P à d Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.

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/clone lib="NCI CGAP Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sal1; Site 2: Not1; Cloned unidirectionally. Primer: Öligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GCTCTGAAATCTAAGAAGATATGTAAATCACTGAAGA-TTGTGGACTAGTG-TTGGTATC 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGCCCTAACTCTAATTGTCCTGTTTTGGGGGGGGCAAGCACTTCTGGCCGGAGGTACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 ACATTGGAAGTCCATGACTTTAAAAATGGATACACTGGCATCTACTT-GTAGGTCTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355 AAATGCTTTATTAAAACTCAAATCAAAGTGATTCCTGAATTTTTCTGAACCAGAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGAAAACCTATGACATGGAGCACACTTTCTACAGCAACGGCGAGAAGAAGAATTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGGAAATTGATCCTGTGACCCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACATTGGAAGTGCACGACTTTAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATGTTTTATCAAAACTCAGATTAAAGTGATTCCTGAATTTTTCTGAACCAGAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTCTGGAGATTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAGAAAAGCCTATGGAAAACAGAGACTTCCTGAAAATTCTAAAATTCTGGAGATTTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATAATGTGACCATGTACTGGATCAATCCCACTCTAATAGCAGTTTCAGAATTACAGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTGAGGAGGACGGTGAAAGATCTTCACTTTTCCTACCAGTGAACACAAGGGGGATGACC
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can letond through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9191 row: i column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 463.6; DB 10; Length 888;
Pred. No. 6.5e-79;
0; Mismatches 114; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH108"
                                                                                                                                    Plate: LLAM9191 row: i column: 20 High quality sequence stop: 677.
                                                                                                                                                                                                              1. .888
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:3986395"
                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 18:7%; 11 Similarity 83.6%; 632; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                653
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465 bp mRNA linear EST 28-NOV-1994
A533F Heart Homo sapiens cDNA clone A533 similar to Chondromodulin,
mRNA.sequence.
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                                                                                               GICGICICAICATGCCITGTAACTGGTGGCCCGCATGCTGGGGAGGGTCTAATAGG 1016
                                                                                                                                                                                                                                                                          1077 AATTICTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCTCTCCAGAATTACTTGTAGGT 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="E.coli Y1090"
/clome_lib="Heart"
/note="Vector: Lambda gtll; Site_l: EcoRI; Site_2: EcoRI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             461 AATTTCTGAACCAGAAGAAAAAAAAAAGAATGAGAATGAAGAAATTACCACAACTTTC-TTGA 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              511 ACAGTCAGTGATTTGGGTCCCAGCAGAAAGCCTATTGAAAACCGAGATTTTCTTAAAAA 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liew,C.C., Hwang,D.M., Fung,Y.W., Laurenssen,C., Cukerman,E.,
Tsui,S. and Lee,C.Y.
A catalogue of genes in the cardiovascular system as identified by
                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 465)
                                                                                                                                                                                                                                                                                                      102 AATTICTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCTCTCCAGAATTACTTGTAGGT 43
                                282 GIGAACCTITACTAGGCIACTACCCAIATCCAIACTGCIACCAAGGAGGAGGAGTCTCT
                                                                                                                                           Grecricretearecerreraacregregeregeceeerrecregeaggeerraarage
                                                                                                                                                                                       2; Gaps
         GTGAACCTTTACTAGGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 91, 10645-10649 (1994)
95024171
                                                                                                                                                                                                                                                                                                                                                                         1137 AATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCA 1176
                                                                                                                                                                                                                                                                                                                                                                                                     Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cliew@rics.bwh.harvard.edu
Similar to bovine chondromodulin
Seg primer: GGTGGCGACGACTCCTGGAGCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .465
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="A533"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Contact: Liew CC
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                    897
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Matches
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MEDLINE
PUBMED
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T12179/c
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KEYWORDS
SOURCE
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// Joine | 11b="Scares NSF F8 9W OT PA P S1"
// Joine | 11b="Scares NSF F8 9W OT PA P S1"
// Joine | 11b="Scares NSF F8 9W OT PA P S1"
// Joine | 11b="Scares NSF F8 9W OT PA P S1"
// Joine | 12b="Scares NSF F8 9W OT PA P S1"
// Joine | 12b="Scares NSF F8 9W OT P S1"
// Equal amounts of plasmid DNA from five normalized
| Libraries were mixed, and ss circles were made in vitro.
| Pollowing HAP purification; this DNA was used as tracer in a subtractive hypridization reaction. The driver was pct-amplified CDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneLDs: Scares NBAFF pool 1:
| 145032-147335, 147720-148103, 148872-149255, 15002 - 154407, 151176-15237 Scares NBAFF Py pool 1:
| 145032-147335, 12174-774407 Scares NBHPA pool 1:
| 158280-760583, 772104-774407 Scares NBHPA pool 1:
| 723720-726407, 139080-74099 Subtraction by Bento
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711 AAAATGAACAGTGGTGGTCCCTCAAGTGAAGTAGAAGAAGACCGGTCACGCCAGACAAG 770
                                            653 AAGAATGAGCAAGGTGGTCGCAAGTTGAGGGGGGAAAACCGCCAAACCAGAAAGCAG 712
                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. I (bases 1 to 462)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF439260 462 bp mRNA linear EST 30-MAR-2
nab61h07.x1 Soares NSF F8 9W OT PA P S1 Homo sapiens CDNA clone
IMAGE:3270397 3' similar to TR:Q9UGG Q9UJGO DJ479J7.1 ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL , contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           717 AACAGIGGGIGGTCCCTCAAGIGAAAGIIACAGAAAGACCCGTCACGCCAGACAAGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                               771 CAAGTGAGGAAGAACTTCCAATAAATGACTATACTG 806
                                                                                                                                        713 CGAGGGAAACTTCATTAAAGGACAATATGGCACTG 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soares and M. Fatima Bonaldo."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="IMAGE:3270397"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'mol_type="mRNA"
'db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                    BF439260.1 GI:11451777
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
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BF439260
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BF439260/c
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VERSION
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TITLE
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CCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA 130
                                                                                                                                                                                                                                                           ATATGTAAATCACTTAAGATTTGTGGACTGGTGTTTGGTATCCTGGCCCTAACTCTAATT 190
                                                                                                                           crercagrecreraaageaggaaaggeacegrereggaggaccaregeaaagaar 201
                                                                                                                                                                                                   CCTCCAGAGAACTGTGAGGGCTGTCACATTCTAAATGCAGAAGCTCTGAAATCTAAGAAG 261
                                                                                                                                                                                                                                                                                                     ATAIGIAAAICACIGAAGAITIGIGGACIAGIG-IIGGIAICCIGGCCIIAACICIAAIT 320
                                                                                                                                                                                                                                                                                                                                                    GICCIGITITIGGGGGAGCAAGCACTICIGGCCGGAGGIACCCAAAAAAGCCTAIGACAIG 250
                                                                                                                                                                                                                                                                                                                                                                                              GAGCACACTITCTACAGCAATGGAGAAGAAGAAGAATTTACATGGAAATTGATCCTGTG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAGCACACTITICIACAGCAACGCGAGAAGAAGAAGAITTACAIGGAAAITGAICCCAIA 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         560 CAAATCAAAGTGATTCCTGAATTTTCTGAACCAGAAGAAGAATAGATGAGAATGGGAGAA 619
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                 311 ACCAGAACTGAAATATTCAGAAGGGGAAATGGCACTGATGAAAACATTGGAAGTGCACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTAAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTACCACACATTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAA
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information of found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM41 row: m column: 14
High quality sequence stop: 422.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CB317710 741 bp mRNA linear ES'AGENCOURT_12263597 NIH_MGC_165 Mus musculus cDNA clone
IMAGE:30281869 5', mRNA sequence.
           Pred. No. 1.9e-71;
0: Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Leslie L. Heckert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACCGAGATTTTCTTAAAATTCCAAAATTCTG 583
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                                       0; Mismatches
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CB317710.1 GI:28841945
             89.5%;
                                     Conservative
             Similarity
             Local Simi
hes 513;
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VERSION
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CB317710
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TITLE
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601759641F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:4022674 5',
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402 ACAGTCAGTGATTTGGGTCCCAGCAGAAAGCCTATTGAAAACCGAGATTTTCTTAAAAA 343
                                                                                                                                                                            ATCAGTCTCTGAGTTACAAGACTTTGAGGAGGAGGAGAAGATCTTCACTTTCCTGCCAA 223
                                                                                                                                                                                                                                                         TGGAATAGAATTTGATCCCATGCTGGATGAGAGGTTATTGTTGTATTTACTGCCGTCG 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: Gapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/Link at:
http://inage.llnl.gov
Plate: LiAM9280 row: a column: 11
High quality sequence stop: 703.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="INAGE:4022674"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
/lab_host="DH10B"
/clone lib="NCI CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH.
                                                                                                                                  631 AICAGTITCIGAGTTACAAGACTTTGAGGAGGAGGAGAAGAICTTCACTTTCCTGCCAA
                                                                               CGAAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGCTCCTCAAGTGAAAGTAGAGAA
                                                                                                                                                                                                                                                                                                                 GACCCGTCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTGAAAA
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGCAACCGCTATTGCCGCGCGTCTGTGAACCTTTACTAGGC 913
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'strain="C57BL/6J"
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Mus musculus
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EST.
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SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

DEFINITION RESULT 37 BF123957 LOCUS

ACCESSION VERSION KEYWORDS EST 04-MAR-2003

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Query Match

source

FEATURES

ORIGIN

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GCCTATGAGGCATCTGGCCCCTGGTAGCCAGCTCTCCAGAATTACTTGTAGGTAATTCCT 1143
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                                                                                                                                                                                                                                                           http://www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=462 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany
Tal: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
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   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 521)
Henrich, J., Hermanns, J., Kranz, H., Loebbert, R., Schlueter, T., Radelof, U., Schneidel, M., Heil, O., Ebert, L., Neubert, P., Peters, M., Radelof, U., Schneider, D. and Korn, B.
Mouse ArrayTaG CDNA (LION)
Contact: Ina Rolfs
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                                                                                                                                                                           GmbH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 521;
                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information.
RP: CAGGAAACAGCTATGAC.
                                                                                                                                                                  RZPD Deutsches Ressourcenzentrum fuer Genomforschung
Im Neuenbeimer Feld 580, D-69120 Heidelberg, Germany
RZPD; LIONP462G08420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 409.4; DB 13;
Pred. No. 1.9e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="LIONp462G08420"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1...521
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87.9%;
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Mus musculus
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                                                                  /tissue_type="primary cultures of Sertoli cells"
/lab host="DH10B (T1-phage-resistant)"
/clone lib="NUH MGC 165"
/clone lib="Organ restis; Vector: pDNR-LIB; Site l: Sfil
/note="Organ restis; Vector: pDNR-LIB; Site l: Sfil
/ggccattatggcc); Site 2: Sfil (ggcgcctcggcc); 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5' -ACACGGCCATATGGCC.3' and 3' adaptor sequence:
5' -ATTCTAGAGGCGCGACGGCATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.4 kb
(range 0:6-3:5 kb). 15/15 colonies contained inserts by
PCR. This library was enriched for full-length clones and
was constructed by Clontech Laboratories (Palo Alto, CA).
Note: this is a NIH_MGC Library."
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s musculus cDNA clone LIOND462G08420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                431 CAGATTAAAGTGATTCCTG-AATTTTCTGAACCAGAAGAGGGAAATAGATGAGAATGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        520 AAATTACTTACAÁCTTÍTÍCTÍTTGÁÁCAGTCÁGTGGAÍTTGGGGTTCCCGGCGAAAAAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 490 AATTACC---ACAACTITCTTTGAACAGTCAGTGATTT---GGGTCCCAGCAGAAAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 ATATGTAAATCACTGAAGATTTGTGGACTAGTGTTTGGTATCCTGGCCTTAACTCTAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATATGTAAATCACTTAAGATTTGTGGACTGGTGTTTGGTATCCTGGCCCTAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                     7; Gaps
                                                                                                                                                                                                                                                                                                                                               35.0%; Score 419; DB 14; Length 741; 88.7%; Pred. No. 2.4e-70; ive 0; Mismatches 55; Indels
       organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX638501 521 b
BX638501 pBluescript Lion Mus
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BX638501
                                                                                                                                                                                                                                                                                                                                                                      al Similarity 88.7
489; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 544 TATTGAAAACC 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATTTGGAAAC 590
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Best Local S
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BX638501/c
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                           EST 05-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Context: Robert Strausberg, Ph.D.
Email: Cgapbs-remail.nih.gov
Tissue Procurement: Dr. David Rowe
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution information can be http://image.llh.gov
http://image.llh.gov
High quality sequence start: 86
High quality sequence start: 86
High quality sequence stop: 334.
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II Hawc http://wgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                         41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by, David Rowe. Library constructed by ResGen, Invitrogen Corp."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243
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                 131 ATAIGTAAATCACTTAAGATTIGTGGACTGGTGTTTGGTATCCTGGCCCTAACTCTAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 ATAIGTAAATCACTGAAGATTTGTGGACTAGTGTTTGGTATCCTGGCCTTAACTCTAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTCAGTCCTCTCAAAGCA-AGGAAAGAGTACTGTGTGCTGAGAGCCATGGCAAAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 14; Length 1224;
                                                                                                                                                                                                                                                                                                CB202990 12290775 NIH MGC 135 Mus musculus cDNA clone IMAGE:30139809 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77; Indels
                                                                                                 1140 TCCTCTCTTCATGTTCTAATAAACTTCTACATTATCA 1176
                                                                                                                                      40 TCCTCTCTTCATAAAACTTCTACATTATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 379.8; DB 1. Pred. No. 6.5e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                            CB202990.1 GI:28238967
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85.0%;
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Matches 47
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ORGANISM
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TITLE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1080 ITCIGCCIAIGAGGCAICTGGCCCCTGGIAGCCAGCTCTCCAGAAITACTIGTAGGIAAT 1139
                                                                                                                                      AI039039
399 bp mRNA linear EST 30-JUN-199 ox30b10.s1 Soares_total_fetus_Nb2HF8-9w Homo sapiens cDNA clone IMAGE:1657819 3' similar to SW:CHMI_BOVIN P17404 CHONDROMODUIN-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          839
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (base 1 to 399)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399 AAGAACTTCCAATAAATGACTATACTGAAAATGGAATAGAATTGATCCCATGCTGGAGG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (infoamage.llnl.gov) for further information. Seq primer: -40mul Fwd. ET from Amersham
High quality sequence stop: 389.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339 AGAGAGGTTATTGTTGTTGTGCCGTCGAGGCAACCGGTATTGCCGCCGCGCTCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      780 AAGAACTICCAATAAATGACTATACTGAAAATGGAATAGAATTTGATCCCATGCTGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAGAGGITATIGITGTATITACTGCCGTCGAGGCAACCGCTATIGCCGCCGCGGTCTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 GIGICATCATGCTIGITALITAGTGGTGGCCCGCATGCTGGGAGGAGGTCTAATAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     159 TITIGAGCICAAATGCITAAACTGCTGGCAACATATAATAATGCATGCTATTCAATGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.2%; Score 385; DB 9; Length 39 larity 99.7%; Pred. No. 9.5e-64; Conservative 0; Mismatches 0; Indels
CTCTTCATGTTCTAATAAACTTCTACATCATCAAAAA 1
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
                                                                                                                                                                                                                      PRECURSOR ;, mRNA sequence.
                                                                                                                                                                                                                                                                            AI039039.1 GI:3278233
                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Best Local Similarity
Matches 396; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="NCI CGAP Mam1"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sal1;
Site 2: Not1; Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Nammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAWR768 row: i column: 12
High quality sequence stop: 581.
High quality Sequence stop: 581.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 733)
                                                                                                             311 ACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGAC 370
                                                                                                                                                                          429
                                                                                                                                                                                                ACCAGAACAGAAATATICAGAAGTGGAAATGGCACTGATGAAACATTGGAAGTCCATGAC 423
 TTTAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATG-TTTTATCAAAAC
                                                                                                                                                                                                                                     TCAGATTAAAGTGATTCCTGAATTTTCTGAACCAGAAGAGGAAA-TAGATGAGAATGAAG
                                                                                                                                                                                                                                                                  484 rccaarcaaagrgarrccrgaarrrrcrgaacccgaggaagaaarrrrargacaargarg
                                                                                                                                                                                                                                                                                                                            544 AATTTACCACCACTTTTTTTCGAACAGTCTGAGCATTTGGGTTCTCGCACGAAAACCCTA
                                                                                                                                                                                                                                                                                                 AAATTACCACACACTTTCTTT---GAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTA
                                                   GAGCACACTITICTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="10 months, virgin"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3594323"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
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DB 10; Length 733;

31.6%; Score 378.6;

Query Match

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AI146280

qb87bi0.xl Soares fetal heart NbHH19W Homo sapiens CDNA clone IMAGE:1707067 3' Similar to SW:CHMI_BOVIN P17404 CHONDROMODULIN-I PRECURSOR;, mRNA sequence.
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1 (bases 1 to 460)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                       107
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 825 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 450.
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                                                     GCTGAGAGACCATGGCAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATG
                                                                                                                                        108 CAGAAGCITTTAAATCCAAGAAAATATGTAAATCACTTAAAGATTTGTGGACTGGTGTTT-
                                                                                                                                                                 GGTACCCAAAAAAGCCTATGACATGGAGCACACT-TTCTACAGCAATGGAGAAGAAGA
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                                                                                               GCTGGGAGACCATGGCAAAGAATCCTCCAGAGAACTGTGAGGGCTGTCACATTCTAAATG
               14; Gaps
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Pred. No. 1.3e-62;
Mismatches 94; Indels
                   0; Mismatches
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  83.3%;
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Unpublished (1997)
                      Matches 539; Conservative
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Animal Genetics Division
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Matches 422; Conservative
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Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H. and Sugimoto,Y.
                                                                                                                                                                                                                                                                                                                                                    AGACTGAAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGGTTATTGTTGTTGTTTT 319
                                                                                                                                                                                                                                                                                                                                                                                           258 CATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTGTGTCATCATGATCTTGTAACT 199
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                                                                                                                                                                                                                                                                                  Length 460;
                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                 31.4%; Score 376.4; DB 9; 99.7%; Pred. No. 4e-62;
                                                                                                                                                                                                                                                                                                      0; Mismatches
                       organism="Homo sapiens"
                                         /db_xref="taxon:9606"
/clone="IMAGE:1707067"
 Location/Qualifiers
                                  mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1161 AACTTCTACATTATCACC 1178
                                                                   sex="unknown"
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AV593196.1 GI:9708353
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Best Local Similarity 99.77
Matches 377; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              990 CCCGCATGCTGGGGAGGGTCTAATAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGG--- 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1047 -CAACATATAATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCCT 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 GAGGCAACCGCTACTGTCGCCGCGTCTGTACTTTACTAGGTTACTACCCGTATCCAT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ø
Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000 bovine ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Bos taurus cartilage fetus"
/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly
was deleted from a Not1 site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          753 CCCGTCACGCCAGACA---AGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAAAAAGGGATTGAACAAAATGAACAGTGGGTCCCTCAAGTGAAAGTAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         468 AAAAAAAAGGCATTGAACAAAACGAGCAGTGGTGGTCCCTCAAGTGAAGGTGGAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           810 ATGGAATAGAATTTGATCCCATGCTGGATGAGAGGTTATTGTTGTATTACTGCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         870 GAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              930 ACTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATGCCTTGTAACTGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 CCAACATATAACAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATTTGGCTCCT
                                                                                                                                                                                          Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Eax: 81-248-25-5725
Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                                   Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.0%; Score 371.6; DB 9; 90.2%; Pred. No. 3.3e-61; ive 0; Mismatches 39;
                                                                        Nucleic Acids Res. 29 (22), E108 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="cartilage"
/dev_stage="fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9913"
/clone="ElCA006A12"
                                                                                                                                              Contact: Yoshikazu Sugimoto
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421 AGCAATGGGTGGT 433
                                                          RESULT 46
AI112003/c
                                                                                                LOCUS
DEFINITION
                                                                                                                                                                                                                                     ORGANISM
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COMMENT
                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
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                                                                                                                                                                                             KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                               VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="adurway or parenchyma"
/dev_stage="adult"
/clone_lib="Rat lung airway and parenchyma cDNA libraries"
/note="Organ: lung; Vector: pGEW-112f(-); Site 1: Eco RI;
Site 2: Not I; mRNA was isolated from microdissected rat
lung airways and parenchyma tissues."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 Argagaargaagaaarracracaacgricririgaacagricagrgarrigggriccrgcag 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAAGCCTATTGAAAACCGAGATTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATA 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GCTTTATTAAAACTCAAATCAAAGTGATTCCTGAATTTTCTGAACCAGAAGAGGAAATAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 597 ACGIGACCAIGIAITGGATCAATCCCACTCTAATAICAGTTTCTGAGTTACAAGACTTTG 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 417 GITITIATCAAAACTCAGAITAAAGTGAITCCTGAAITTTTCTGAACCAGAAGAGGAAATAG 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 AAAAGCCTATTGAAAACAGAGACTTCCTGAAAATTCTAAAATTCTGGAGATTTGCGACA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 AAATTGATCCTGTGACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACAT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                         Average Phred score is 20 or better. All poor quality data (Phred 20) and vector/linker sequence has been removed. High quality sequence stop: 433. Location/Qualifiers
                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAATTGATGCCATAACCAGAACAGAATATTCAGAAGTGGAAATGGCACGATGAAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGAAGTGCACGACTTTAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 433)
Shultz,M.A., Zhang,L., Gu,Y.-Z., Baker,G.L., Fannuchi,M.V.,
Shultz,M.A., Gurke,W.A., Morin,D., Penn,S.G., Jovanovich,S.B.,
Plopper,C.G. and Buckpitt,A.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                        Dept. of Molecular Biosciences, School of Veterinary Medicine University of California, Davis
1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA Tel: 530 752 0793
Fax: 530 752 4698
Email: mashultz@ucdavis.edu
                                                                                                                                                                                                   Gene Expression Analysis in Response to Lung Toxicants: I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 30.8%; Score 369; DB 14; Length 433; al Similarity 90.8%; Pred. No. 1.1e-60; 393; Conservative 0; Mismatches 40; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Rattus norvegicus"
                                                                                                                                                                                                                 Sequencing and Microarray Development Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="CA2448"
                            Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            717 AACAGTGGGTGGT 729
                                                                                                                                                                                                                                                                Contact: Shultz MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .433
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                                SOURCE
ORGANISM
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                                                                                                                               REFERENCE
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                KEYWORDS
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/download_lib="UILPR-Y0"
/clone_lib="UILPR-Y0"
/clone_lib="UILPR-Y0"
/clone_lib="UILPR-Y0"
/note="Toector: pr773D-Pac (Pharmacia) with a modified
/note="Toector: pr773D-Pac (Pharmacia) with a modified
polylinker; Site_l: Not I; Site_2: Eco RI; The UI-R-Y0
library is a subtracted library derived from an individually-tagged normalized whole-eye (minus the lens)
library. The driver for the subtraction consisted of a
pool of all previous libraries (UI-R-AU, UI-R-AI, UI-R-B0,
UI-R-EI, UI-R-C0, and UI-R-C1). The tag is a string of
UI-R-EI, UI-R-C0, and UI-R-C1). The tag is a string of
oligo-dr track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-Y0) was constructed as follows: PCR
amplified cDNA inserts from previous library clones from
which 3' ESTS had been derived were used as a driver in a
hybridization with the normalized whole-eye library in
the form of single-stranded circles. Subtracted the labrary in
the form of single-stranded circles subtromatography, converted to
double-stranded circles and electroporated into DH10B
bacteria (Life Technolquies) to generate the UI-R-Y0
library: This procedure has been previously described
(Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence tag present in the cDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized adult Eye library. cDNA Library Preparation: M. Fatima Bonaldo. Ph.D. Clone distribution: clones will be available through Research
                                    EST 11-FEB-1999
                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 487)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
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487 bp mRNA linear EST 11-F.
UI-R-YO-mp-b-11-0-UI.81 UI-R-YO Rattus norvegicus cDNA clone
UI-R-YO-mp-b-11-0-UI 3', mRNA secuence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA 781: 319 335 9565 Email: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.6%; Score 366.8; DB 9; Length 487;
86.9%; Pred. No. 2.7e-60;
iive 0; Mismatches 52; Indels 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             forganism="Rattus norvegicus"
/mol type="mRNA"
/mol type="mRNA"
/strain="Sprague-Dawley"
/db xref="taxon:10116"
/clone="Ulr.R-V0-mp-b-11-0-UI"
/dev stage="adult"
/lab host="NH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                                            Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: M13 Forward.
Location/Qualifiers
                                                                                                                                                   AI112003 TAI112003.1 GI:3511952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 86.9
Matches 431; Conservative
                                                                                                                                                                                                                                                                                                   Rattus norvegicus
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Best Local Similarity
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1004 AGGGICIAATAGGAGGTTTGAGCTCAAATGCTTAAACTGCT----GGCAACATATAATAA 1059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGAATTACTIGTAGGIAATTCCTCTTCATGTTCTAATAAACTTGTACATTATCACCA 1179
                                                                                                   CAGAATTATTTGTAGGATATTCCTCTTCTTCTATTAAACGTCTACATCATCATCA
                                                                         GATCCCATGCTGGATGAGAGGTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTAT
AGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTGAAAATGGAATAGAATTT
                                 AGACAAGCAAGCGAAGACCTTCCTGTTAATGACTATACTGAAAATGGAATCGAATTT
                                                                                                                                                     TGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATACTGCTACCAAGGA
                                                                                                                                                                            247 GGTCGAGTCATCTGTCATCATGCCTTGCAACTGGTGGCCGCCGCATGCCTTGGG
                                                                                                                                                                                                                                                                                                                                         AGAĞTCTAATAĞGAAĞTTTĞAĞTCCAAATĞCTTAACCTTTTGTTAĞCCAACATATAATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1180 AAAAAAAAAAAAA 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          discovery
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764
                                     427
                                                                                                             367
                                                                                                                                                                                                                                                                                                                                           187
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BF523627
UI-R-C1-lc-e-10-0-UI.x1 UI-R-C1 Rattus norvegicus cDNA clone
UI-R-C1-lc-e-10-0-UI 5', mRNA sequence.
BF523627.1 GI:11631594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: bento-soares@uiowa.edu

CDNA Library Preparation: M.B. Soares Lab Clone distribution:

Cones will be available through Research Genetics (www.resgen.com)

This clone is also available through the I.M.A.G.E. Consortium at

LLNL (info@image.llnl.gov). IMAGE ID= 1792597

Seq primer: M13 Forward.
                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                           1 (bases 1 to 504)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA Tel: 319 335 8256 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 6 (9), 791-806 (1996) 97044477
                                          LOCUS
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VERSION
KEYWORDS
SOURCE
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RESULT 47
BF523627
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AUTHORS
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/dov\_stage="Adult"
/dev\_stage="Adult"
/dev\_stage="Adult"
/lab host="MHIOB (Life Technologies)"
/lab host="MHIOB (Life Technologies)"
/lab host="WHIOB (Life Technologies)"
/lote="Vector: pT730-pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; The UI-R-CI
library is subtracted library derived from the UI-R-Dibrary derived from the UI-R-I library of a subtracted library derived from the UI-R-I library, which is a subtracted library derived from the UI-R-I library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, prain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-EI library consisted of a mixture of individually tagged normalized libraries constructed from findividually tagged normalized libraries constructed from of individually tagged normalized libraries constructed from of individually tagged normalized fibrary of a clone within the mixture. The subtracted library of origin of a clone within the mixture. The subtracted library of origin of a clone within the mixture. The subtracted library of origin of a clone within the mixture. The subtracted library as a driver in a hybridization with the UI-R-CO library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-CI library, This procedure has been nreviously described library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806, 1996)" 'strain="Sprague-Dawley"
'db xref="taxon:10116"

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763

ATTGAACAAAATGAACAGTGGTGGTCCCTCAAGTGAAAGTAGAGAGGCCGTCACGCC

704

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Gaps 16; Length 53; Indels DB 10; Score 366.2; DB 1 Pred. No. 3.5e-60; 0; Mismatches 30.6%; 86.5%; 444; Conservative Query Match Best Local Similarity Matches à

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CTCTTCATGTTCTAATAAACTTCTACATTATCA 1176

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A1502787/c
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AİTAĞCAAAACTGAAATATTCAGAAGTGGAAATGGCACTGATGAAACATTGGAAGTACAT 240
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Liang, F., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Reele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                    EST 30-AUG-2001
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                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Fecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from day 20 and day 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AAGATATGTAAATTACTTAAGATTTGTGGATTGGTATTTGGTATCCTCGCCTTAACTCTA
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                                                                           A04 bp mRNA linear 398963 MARC 4BOV Bos taurus cDNA 5', mRNA sequence. BI535434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366
472 CTCTTCGTGTTCTAATAAACGTCTACATCATCA 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Bos taurus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plate: 127 row: B column: 3
Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH108"
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FORWARD: AGGAAACAGCTATGACCAT
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Fax: 402 762 4390
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                                                                                                                                                                                     Bos taurus (cow)
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                                                                                                            DEFINITION
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                                                         RESULT 48
BI535434
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University of Iowa University of Iowa University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA 7e1: 319 335 8250
Fax: 319 335 9565
Email: bento-goares@uiowa.edu
The sequence contained an oligo-dT track that was present in the oligonuclectide that was used to prime the synthesis of first oligonuclectide that was used to prime the synthesis of first oligonuclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A strand cDNA and therefore this may represent the Norl site tail. The sequence tag present in the CDNA between the NotI site and the oligo-dT track served to identify it as a clone from the normalized 18 day embryo library CDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: MIS Forward.
                                                                                                                                                                                                                                                                                                                                               AISO2787
UI-R-C1-10-e-10-0-UI.st UI-R-C1 Rattus norvegicus cDNA clone
UI-R-C1-10-e-10-0-UI 3', mRNA sequence.
                                                                                                                    427
                                                                                            487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 492)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
  368 GACTITAAAAACGGATACACTGGCATCTTCGTGGGTCTTCAAAAATGTTTTATCAAA
                                      428 ACTCAGATTAAAGTGATTCCCGGAAATTTTCTGAACCAGAAGGAAATAGATGAGAATGAA
                                                                                                                                                                                        488 GAAATTACCACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCC 531
                                                                                                                                                                                                                   Coordinated Laboratory for Computational Genomics
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/mol_type="mRNA"
/strain="Sprague-Dawley"
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/clone="UI-R-C1-lc-e-10-0-UI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Norway rat)
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Soares, MB
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library (UI-R-CI) was constructed as follows: PCR amplified cDNA inserts from UI-R-CO clones from which 3 ESTs had been derived was used as a driver in a hybridization with the UI-R-CO library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by

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556; Conservative
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hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the U.R-C1 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B82 bp mRNA linear EST 21-DEC-20
602153429F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294374 5',
mRNA sequence.
                                                                                                                                                                                                                                                                      GAATAGAATTTTGATCCCATGCTGGATGAGAGGTTATTGTTGTTTTACTGCCGTCGAG
                                                                                                                                                                                                                                            ccccccccacacaacaa--caggaagaccrrccrgraargacraracrgaaarg
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                          16;
                                                                                                          30.0%; Score 358.8; DB 9; Length 492; llarity 86.5%; Pred. No. 9.2e-59; Conservative 0; Mismatches 52; Indels 16
                                                                                                                                                                                                                                                                                                                                                                                                                                    GCATGCTGGGGAGGGTCTAATAGGAGGTTTGAGCTCAAATGCTTAAACTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 ACATATAATTAATGCATGCTACTCCATGAATTTCTGCAT
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/clone "IMAGE:4294374"
/lab host="DH10B (T1 phage-resistant)"
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/note="office lib="WHH MGC 83"
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and 3' adaptor sequence: S'-CACGGCCATATGGCC-3'
and 3' adaptor sequence: S'-CACGGCCATATGGCC-3'
C, or G and N = A, C, G, or T). Average insert size l.4
kb (range 0.5-4.0 kb): 14/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA)."
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                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM1143 row: j column: 07
High quality sequence stop: 436.
Location/Qualifiers
Tissue Procurement: CLONETECH Laboratories, Inc. cDNA Library Preparation: CLONETECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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87.7%; Pred. No. 9.1e-59;
iive 0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                  'organism="Homo sapiens"
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/db_xref="taxon:9606"
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Tue Sep 7 12:23:17 2004

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Search completed: September 3, 2004, 09:20:16 Job time : 2377 secs

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(without alignments)
15870.790 Million cell updates/sec
                                                                                                             3, 2004, 04:35:02 ; Search time 3269 Seconds
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                            3470272 seqs, 21671516995 residues
                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                   - nucleic search, using sw model
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em_htg_other: *
em_htg_other: *
em_htg_pln: *
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em_htgo_hum:*
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Maximum DB seq length; 200000000
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Pred. No. is the number of results predicted by chance to have a

PAT 21-MAR-2001

linear

DNA

ALIGNMENTS

1197 bp Sequence 115 from Patent WO0116318. AX092384

DEFINITION

RESULT 1 AX092384 LOCUS

ACCESSION

AX092384.1 GI:13444506

Homo sapiens (human)

VERSION KEYWORDS SOURCE ORGANISM

Homo sapiens

REFERENCE AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
Wood,W.I.

AF191770 Home sapi AF291656 Home sapi AR338895 Sequence AB059407 Equus cab BC049994 Mus muscu BC049994 Mus muscu AF21993 Mus muscu AF21993 Mus muscu BD094022 A novel p AF191769 Rattus no AF191769 Rattus no BC006919 Mus muscu BD094032 A novel pro BD094032 A novel pro BD094032 A novel pro AB055422 Mus muscu AR055423 Rattus no AR203129 Sequence BD094033 A novel pro BD094033 A novel pro BD077399 Novel pro BD077399 Novel pro BD07739 Novel pro BD07739 Novel pro BD07739 Novel pro BD07739 Novel pro BD07739 Novel pro BD07739 Novel pro BD07739 Novel pro BD07739 Novel pro BD07739 Novel pro BD07739 Novel pro BD07740 Novel pro AL691421 Mouse DNA AX884585 Sequence BD024197 Sequence BD204197 S'EST and BD228719 Mammalian Homo sapi 33 human A novel p Mammalian Sequence AC107412 Rattus no BC045152 Mus muscu U43509 Mus musculu Homo sapi AX092384 Sequence AX464390 Sequence Sequence Sequence score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. BD269275 BD228713 AR338896 SUMMARIES AF291655 AF219993 BD094022 BD094023 AF191769 BC006919 AB055423 AX203129 BD094033 BD077399 BD096255 HS47977 AL691421 AX884585 BD024195 BD204197 BD228719 AC107412 BC045152 MMU43509 AF291656 AB055421 AR338895 AB059407 BD077398 BD096254 BD094032 AX697253 AY358706 BD269275 AX203127 BD094021 BD228713 AR338896 AF234259 AF191770 AX203136 BD094036 BD077400 AB055422 AF191768 BD096256 AX092384 **AX464**390 10 10 DB Length 97189 20850 1428 1338 1180 1336 1153 951 951 975 1128 1214 1136 951 432 309 1449 1197 221461 240491 Query Match 29.4 25.8 25.8 25.2 21.6 100.0 100.0 100.0 79.3 79.3 79.3 778.8 31.6 21.6 20.6 115.4 11.2 99.9 83.1 82.1 83,1 1197 1197 1196 1194 1187.2 1178 994.6 982.4 979.2 949.4 949.4 949.4 932.6 926.2 Score 961.8 805.4 805.4 378.8 377.2 352.4 247 184.4 134 130.8 1138.4 No. Result 

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TCTGCCTATGAGGCATCTGGCCCCTGGTAGCCAGCTCTCCAGAATTACTTGTAGTAATT 1140
                                                                                                                                                           TIGAGCICAAATGCITAAACIGCTGGCAACATATAATAAATGCATGCTATICAAATGAATT 1080
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Gao,W.O., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,
Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Wood,W.L. and Zhang,Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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GAGAGGTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCGTCTGTGA
                              ACCTITACTAGGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTCG
                                                Length 1197;
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100.0%; Pred. No. 4.2e-286;
ive 0; Mismatches 0;
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Genentech Inc. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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Sequence 523 from Patent W00140466.
AX464390
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Best Local Similarity 100.
Matches 1197; Conservative
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; Pred. No. 4.2e-286;
0; Mismatches 0;
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Patent: WO 0116318-A 115 08-MAR-2001;
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                                                       i, Inc. (US)
Location/Qualifiers
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Matches 1197; Conservative
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ilarity 100.0%; Pred. No. 4.2e-286;
Conservative 0; Mismatches 0;
                                                                                                 Patent: WO 0078961-A 321 28-DEC-2000;
Genentech Inc. (US)
Location/Qualifiers
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Best Local Similarity
Matches 1197; Conserv
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AX697253 1197 bp | Sequence 321 from Patent W00078961. AX697253. GI:29498415

RESULT 3
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM

. Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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                                                                                                   Length 1197;
                                                                                                                           Indels
                                                                                                     Query Match
100.0%; Score 1197; DB 9;
Best Local Similarity 100.0%; Pred. No. 4.2e-286;
Matches 1197; Conservative 0; Mismatches 0;
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llarity 100.0%; Pred. No. 7.5e-286;
Conservative 0; Mismatches 0;
              /mol_type="genomic DNA"
/db_xref="taxon:9606"
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Matches 1196;
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2P 2002334972-A/10
2P 200234972-A/10
1B-2000 UP 2000594904
19-JAN-1999 US 60/116330
CRAIG A ROSEN, STEVEN M RUBEN, REINHARD EBNER, PAUL E YOUNG, JIAN
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SERVICES STEENCES INC.

PN JP 2002534972-A/10

PD 22-OCT-2002

PP 18-JAN-2000 JP 2000594904

PR 19-JAN-1999 US 60/116330

PI CRAIG A ROSEN, STEVEN M RUBEN, REINHARD EBNER, PAUL E YOUNG, JP INI,

PR NJ MACORE, GEORGE KOMATSOULLS, CHARLES E BIRSE PC C12N15/09, A61K31/7115, A61K35/76, A61K38/00, A61K45/00, A61K48/00,
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                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 1178)
Lok, S. and Presnell, S. R.
Lok, S. and Presnell, S. R.
Mammalian chondromodulin-like protein
Patent: JP 2005330078-A 1 17-SEP-2002;
ZYMOGENETICS INC
      AGAACTTCCAATAAATGACTATACTGAAAATGGAATAGAATTTGATCCCATGCTGGATGA
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Home sapiens (human)
Home sapiens (human)
TP 2002530078-A/1
17-SEP-2002
12-NOV-1999 UP 2000582562
13-NOV-1999 US 09/191986
13-NOV-1999 US 09/191986
21 inc. SCOTT R PRESNELL
2 CI2N15/09, CO7K14/51, C07K16/24, C12N15/00
C Mammalian chondromodulin-like protein
H Key Location/Qualifiers
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100.0%; Pred. No. 2.2e-281;
iive 0; Mismatches 0;
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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BD228713.1 GI:33038483
JP 2002530078-A/1.
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Matches 1178; Conservative
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R 29-SEP-1999 JP 99P 275947

I KEI YAMANA, YUKIMI TAKAHASHI, HITOSHI WADA, YOSHINORI KASAHARA

C12N15/12, C12Q1/68, C12P21/08, C12N1/15, C12N1/19, C12N1/21, C12N5/
      1 (bases 1 to 1200)
Yamana, K., Takahashi, Y., Wada, H. and Kasahara, Y.
A novel polypeptide and its encoding gene
Patent: WO 0123557-A 1 05-APR-2001;
TEIJIN LTD, KEI YAMANA, YUKIMI TAKAHASHI, HITOSHI WADA, YOSHINORI
KASAHARA
OS Homo sapiens (human)
PN WO 0123557-A/1
PD 05-APR-2001
PP 25-SEP-1999 JP 99P 275947
PR 22-SEP-1999 JP 99P 275947
PI KEI YAMANA, YUKIMI TAKAHASHI, HITOSHI WADA. YOSHINORI KAGAHAD
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99.2%; Score 1187.2; DB 6; Length 1200;
Best Local Similarity 99.7%; Pred. No. 1.1e-283;
Matches 1189; Conservative 0; Mismatches 3; Indels 0;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Location/Qualifiers

    .1200
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    /mol_type="genomic DNA"
    /db_xref="taxon:9606"

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2 AGCAGTGGTCTCTCAGTCCTCTCAAAGCAAAGCATACTGTGTGTG	Oy         842 AGAGGTATTGTTGTTTACTGCCGTCGAGGCAACCGCTATTGCCGCCGCGTCTGTGAA 90.1           Db         841 AGAGGTTATTGTTGTATTACTGCGGTGGGGGGAACCGCTATTGCCGCCGTCTTGTGAA 900           Oy         902 CCTTTACTAGGCTACTACCCATATCGCTACCAAGGAGGACGAGTCATTGTCGT 96.1           Oh	962 GTCATCATGCCTTGTAACTGGTGGCTGCCTACTGGGGAGGGTCTAATAGGAGGTT 962 GTCATCATGCTTGTAACTGGTGGCTGCCTGCTGGGGAGGGTCTAATAGGAGGTT 961 GTCATCATGCTTGTAACTGGTGGGTGCCCGCATGCTGGGGAGGGTCTAATAGGAGGTT 1022 TGAGCTCAAAACTGCTGGAACATATAATAAAATGCTAATAATAATATAATAATATAATATAATATAAATTTTAATAAATTTT	

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Shukunami, C., Oshima, Y. and Hiraki, Y.
Direct Submission

Direct Submission

Direct Submission

Institute (14-FEB-2000) Molecular Interaction & Tissue Engineering, Institute for Frontier Medical Sciences, Kyoto University, 53 Shogoin-Kawahara-cho, Sakyo-ku, Kyoto 606-8507, Japan

Location/Qualifiers
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              GACCATGTATTGGATCAATCCCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGA
                                    AGAACTTCCAATAAATGACTATACTGAAAATGGAATAGAATTTGATCCCATGCTGGATGA
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Shukunami, C., Oshima, Y. and Hiraki, Y.
Molecular cloning of tenomodulin, a novel chondromodulin-I
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/db_xref="taxon:9606"
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Homo sapiens tenomodulin mRNA,
AF234259
AF234259.1 GI:12231526
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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2 (bases 1 to 1309)
Leclerc.L., Cros.N. and Dechesne, C.A.
Direct Submission
Submitted (04-0CT-1999) Faculte des Sciences, CNRS UMR 6548, Par Valrose, Nico 66108, France
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Cros,N., Tkatchenko,A.V., Leclerc,L., Leger,J.J., Marini,J.-F.
Dechesne,C.A.
                                                                                                                                              ATGCTTAAACTGCTGGCAACATATAATAATGCATGCTATTCAATGAATTTCTGCCTATG
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                                         GGCTACTACCCATATCCATACTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATG
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/tisaue_type="leg skeletal muscle"
187. .1140
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Pred. No. 3.8e-280;
); Mismatches 5;
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Homo Sapiens myodulin mRNA, complete cds.
AF191770
AF191770.1 GI:11065923

    .1309
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Kiyoki, M.
Molecular cloning and characterization of CHMIL, a novel membrane
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/brotein_id="Aak83109.1"
/dx xxef="id:115077276"
/translation="waknoPperceDGHILNAEAFKSKKICKSLKICGLVFGILALTLI
VLFWGSKHFWPEVPKKAYDMEHTFFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEV
VLFWGSKHFWPEVPKKAYDMEHTFFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEV
KPIBNBGTIFVGLQKCFFKTQLIVVTPFSSPEBEIDDEBESTTTFFFSOSVTWPAE
KPIBNBGFLKNSKILASICDNVTWFWINPTLISUSELDPDFEBGEDDHFPANEKGGIEG
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Catarrhini, Hominidae, Homo.
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Brandau,O., Aszodi,A., Meindl,A. and Fassler,R.
Direct Submission
Submitted (30-JUL-2000) Experimental Pathology, Lund University,
Solvegatan 25, Lund 22185, Sweden
Location/Qualifiers
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                                                                                                    AF291656 1184 bp mRNA linear
Homo sapiens chondromodulin-IB mRNA, complete cds.
AF291656
1269 CCTCTCTTCAIGTTCTAATAAACTTCTACATTATCAAAAA 1309
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/product="chondromodulin-IB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                          Homo sapiens
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
                                                                                                                                                                        GI:15077275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="CHM-IB"
                                                                                                                                                                                                           Homo sapiens (human)
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                                                                                                                                                                                                   <u> AGTGAGGAAGAACTTCCAATAATGACTATACTGAAAATGGAATAGAATTTGATCCCATG</u>
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                                              AATGAACAGTGGGTCCCTCAAGTGAAAGTAGAGAAGACCCGTCACGCCAGACAAGCA
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Pred. No. 5.3e-266;
0; Mismatches 5;
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1 (bases 1 to 1428)

Tang, Y. T., Zhou, P. and Drmanac, R.T.
Nucleic acids and polypeptides
Patent: US 6569662-A 386 27-MAY-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 386 from patent US 6569662.
AR338895
AR338895.1 GI:33725752

    11. 1428
    /organism="unknown"
    /mol_type="genomic DNA"

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PDFKNGYTGTYTVGLQKCFIKYQIKYTPESPBEBEBIDBUEBETTTTFFRSGYTWYDAE
KPIENNEFINGSKILEICDNVTWYNNTNPTLISGVSELQDFEBEGEDLHFPANEKKGIEG
NEQWVVPQVKVEKTRHARQASEBELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                          Direct Submission
Submitted (05-FBB-2001) Kei Yamana, Teijin Limited, Teijin
Institute for Biomedical Research; 4-3-2 Asahigaoka, Hino, Tokyo
191-8512, Japan (E-mail:k.yamana@teijin.co.jp,
Tel:81-42-586-8281(ex.8281), Fax:81-42-587-5519)
Location/Qualifiers
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Pred. No. 1.5e-271;
0; Mismatches 1; Indels 0;
                   (2001)
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                   Biophys. Res. Commun. 280 (4), 1101-1106
    similar to chondromodulin-I
                                                                                                                                                                                                                                                                                                                                             /protein_id="BAB21756.1"
/db_xref="GI:12698293"
                                                                                                                                                                                                       'organism="Homo sapiens"
                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                codon_start=1
product="ChM1L"
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/gene="ChM1L"
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Best Local Similarity 99.9%;
Matches 1139; Conservative 0
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ABUS9407 1175 bp mRNA linear MAM 19-SEP-2002
Equus caballus TNMD mRNA for tenomodulin, complete cds.
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BPKRGYTSTYSTYGLGACFIKTGIKTV BESBEBEBIEDBEBETTTTFFSGYSTIWPAB
KPIENKDFLKNSKILESICDNVTMWWINPTLIAVSELQDFEBGEBLHFPTNDKKGIEG
NEQWVVPQVKVEKTRRARQASEEELPINDYTENGIEFDPMLDERGYCCIYCRRGNRYC
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                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (05-APR-2001) Telhisa Hasegawa, JRA Equine Research
Institute, Laboratory of Molecular and Cellular Biology; 321-4
Tokami-Cho, Utsunomiya, Tochigi 320-0856, Japan
(B-mail:telhisab@enter.equinst.go.jp, Tel:81-28-647-0662,
Fax:81-28-647-0686)
On Sep 19, 2002 this sequence version replaced gi:15982572.
Location/Qualifiers
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                                                                                                                                                                                                                Equus caballus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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Pred. No. 4.9e-248;
0; Mismatches 69;
       1273 ITCIAATAAACTICTACAITAICACCAACA 1302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Equus caballus"
/mol_type="mRNA"
/strain="Thoroughbred"
/db_xref="taxon:9796"
/tissue_type="tendon"
/dev_stage="adult"
/note="domestic horse"
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2 (bases 1 to 1175)
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/gene="TNMD"
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Best Local Similarity 93.8%;
Matches 1099; Conservative
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